

STIC-Biotech/ChemLib

100897

From: Sullivan, Daniel
Sent: Tuesday, August 12, 2003 8:23 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search for 10023530

Please search for the following in the commercial and issued patent databases:

-A nucleic acid comprising the sequence set forth as SEQ ID NO: 1 OR 3-

Thank you.

Daniel M. Sullivan
Examiner AU 1636
Room: 12D12
Mail Box: 11E12
Tel: 703-305-4448

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 8/13
Date Completed: 8/21
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 05:08:13 ; Search time 197.915 Seconds
(without alignments)
8961.061 Million cell updates/sec

Title: US-10-023-530-1

Perfect score: 657
Sequence: 1 atgagccgcgcagggcggt.....gacagattattcaaac 657

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_15Jun03.*

1: /SIDSI/gcgdata/geneseq/emb1/NA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/emb1/NA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/emb1/NA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/emb1/NA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/emb1/NA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/emb1/NA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/emb1/NA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/emb1/NA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/emb1/NA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/emb1/NA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/emb1/NA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/emb1/NA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/emb1/NA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/emb1/NA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/emb1/NA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/emb1/NA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/emb1/NA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/emb1/NA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/emb1/NA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/emb1/NA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/emb1/NA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/emb1/NA2001A.DAT:*
23: /SIDSI/gcgdata/geneseq/emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/emb1/NA2002.DAT:*
25: /SIDSI/gcgdata/geneseq/emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	657	100.0	657	24	ABK86903
2	657	100.0	1707	20	AAA73132
3	657	100.0	2151	20	AAK86501
4	657	100.0	2151	21	AAAS1229
5	657	100.0	2151	21	AAZ93350
6	657	100.0	2151	21	AAZ93710
7	657	100.0	2151	22	AAK84610
8	657	100.0	2151	24	AAK41041

9	657	100.0	2151	24	ABBS1009
10	655.4	99.8	2419	21	AAZ29233
11	652.2	99.3	3220	22	AAH90079
12	610.2	92.9	2285	22	AAK51715
13	610.2	92.9	2285	22	AAK51717
14	610.2	92.9	3622	22	AAH89966
15	608.6	92.6	3003	22	AAK52699
16	608.6	92.6	3003	22	AAK52700
17	608.6	92.6	3003	22	AAK52701
18	564.2	85.9	1707	21	AAK73131
19	564.2	85.9	2175	21	AAZ93714
20	532.4	81.0	2207	22	AAK51716
21	492	74.9	1561	22	AAK84601
22	256.2	39.0	951	23	ABK43155
23	256.2	39.0	2084	22	AAI61150
24	256.2	39.0	4230	21	AAAS1228
25	256.2	39.0	4344	22	AAK52260
26	256.2	39.0	4360	22	AAI59364
27	193.2	29.4	547	24	ABN73551
28	186.2	28.3	2387	23	ABL06081
29	124.4	18.9	126	20	AAK35523
30	124.4	18.9	126	22	AAI14858
31	108.8	16.6	9129	23	ABL06080
32	78	11.9	413	22	AAK53244
33	60	9.1	60	24	ABN41632
34	36.2	5.5	129021	21	AAZ34737
35	35.6	5.4	16941	21	AAZ22996
36	35.4	5.4	12286	24	AAK98748
37	35.2	5.4	511	24	ABQ47110
38	35.2	5.4	511	24	ABQ47111
39	35	5.3	29828	15	AAO73589
40	34.6	5.3	1848	23	ABL11606
41	34.6	5.3	2246	10	AAO73589
42	34.6	5.3	2246	16	AAO74064
43	34.6	5.3	2246	19	AAV48290
44	34.6	5.3	2246	19	AAV48291
45	34.6	5.3	2246	19	AAV48288

ALIGNMENTS

RESULT 1	ABK86903	standard; DNA; 657 BP.
ID	ABK86903	
NC	ABK86903;	
XX		
DT	24-SEP-2002 (first entry)	
DE	Human beta TrCP (bTrCP) bait gene sequence.	
XX		
KW	Human: beta TrCP; bTrCP; protein-protein interaction complex; Ras SFL;	
KW	drug screening; selected interacting domain; SID; tumour; gene therapy;	
KW	bait protein; cytosolic; gene; ds.	
XX		
OS	Homo sapiens.	
XX		
FH		
FT	Key	Location/Qualifiers
FT	CDS	1..657
FT		/tag- a
FT		/partial
FT		/product- "Human beta TrCP (bTrCP) protein"
FT		/note- "this sequence lacks a stop codon"
XX		
PN	W0200250261-A2.	
XX		
PD	27-JUN-2002.	
XX		
PF	18-DEC-2001; 2001MO-EP15414.	
XX		
PR	18-DEC-2000; 2000MS-256276P.	
XX		

PA (HYBR-) HYBRIGENICS.
PA (INRM) INST NAT SANTE & RECH MEDICALE
....

PI Legrain P, Benarous R, Blot G, Lassot I;

DR WPI; 2002-508795/54.
DR P-PSDB; AAU98087.

DR P-PSDB; AAU98087.

DR P-PSDB; AAU98087.

PT Protein-protein complexes for screening drugs or agents that modulate
PT interaction of proteins, e.g. for identifying the selected interacting
PT Domains (SID), comprises interaction between beta-Trcp and Ras Sfl -
XX
PS
CY Claim 2; Page 46-47; 84pp; English.

PS Claim 2; Page 46-47; 84pp; English.

CC The present invention relates to a new complex of protein-protein
CC interaction between betaTRCP (not defined in specification) and Ras SFL
CC The protein-protein complex of the invention is useful for screening
CC drugs or agents that modulate interaction of proteins. In particular,
CC the protein complex is useful for identifying the selected interacting
CC Domains (SID). The modulating compounds detected can be used for
CC treating tumours. The polynucleotides encoding the protein complex may
CC be used in gene therapy. The present nucleic acid sequence encodes the
CC human beta TRCP (btrcp) protein that was used in the methods of the
CC invention as a bait protein.

Sequence 657 BP; 211 A; 131 C; 163 G; 152 T; 0 other;

Query Match	Score	DB	Length
100.08;	657;	24;	657;
100.08;	657;	24;	657;
100.08;	657;	24;	657;

Best Local Similarity 100.0%; Pred. No. 1.1e-201;
Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGAGCCCGGCGAGCGGTGCTGCMAGAGAGGACCTCAATTTATGATATTCCTCAAG	60
Db	1	ATGAGCCCGGCGAGCGGTGCTGCAAGAGGACCTCAATTTATGATATTCCTCAAG	60
QY	61	AGGAAGACTGTAAATAATGCGCAACCCCTAGGAAGATATATCCAGAGAAATTCATT	120
Db	61	AGGAAGACTGTAAATAATGCGCAACCCCTAGGAAGATATATCCAGAGAAATTCATT	120
QY	121	AGACAGACATACAAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTATGTTAGCA	180
Db	121	AGACAGACATACAAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTATGTTAGCA	180
QY	181	AGACATGCTATGAAGACTGAGAATTTGTGGCCAAACAAACTTGGCAATGGCACTTCC	240
Db	181	AGACATGCTATGAAGACTGAGAATTTGTGGCCAAACAAACTTGGCAATGGCACTTCC	240
QY	241	AGTATGATTGTGGCCAAAGCAAGAAACTCTCAGCAAGTATGAAGAAAGAAAGAACTG	300
Db	241	AGTATGATTGTGGCCAAAGCAAGAAACTCTCAGCAAGTATGAAGAAAGAAAGAACTG	300
QY	301	TGTGTCAAAATCTTTGAGCAGTGGTGCAGAGTCAGATCAAGTGAATTTGTGGAACATCTT	360
Db	301	TGTGTCAAAATCTTTGAGCAGTGGTGCAGAGTCAGATCAAGTGAATTTGTGGAACATCTT	360
QY	361	ATTATCCCAATGTGTATTACCAACATATGGGCAATAAACTGCTATCTTAAACCTATGTTG	420
Db	361	ATTATCCCAATGTGTATTACCAACATATGGGCAATAAACTGCTATCTTAAACCTATGTTG	420
QY	421	CAGAGAGATTCATAAATCTGCTGCGACGTCGGGAGTTGGATCATATGCTGAGAACATT	480
Db	421	CAGAGAGATTCATAAATCTGCTGCGACGTCGGGAGTTGGATCATATGCTGAGAACATT	480
QY	481	CTGTCTACTGGAATGCCAAATCAGATATGCTGTGAAACTGCTGTGCAAGAAATGCTATC	540
Db	481	CTGTCTACTGGAATGCCAAATCAGATATGCTGTGAAACTGCTGTGCAAGAAATGCTATC	540
QY	541	CGAGTAGCCTGTATGGCATGCTGTGGAAGAAAGCTTATCGAAGAAATGCTGAGACAGAT	600
Db	541	CGAGTAGCCTGTATGGCATGCTGTGGAAGAAAGCTTATCGAAGAAATGCTGAGACAGAT	600
QY	601	TCCTCTGGAGAGGCGCTGGCAGAAAGAAAGAGATGGGACAGTATTTATTCAAAAC	657
Db	601	TCCTCTGGAGAGGCGCTGGCAGAAAGAAAGAGATGGGACAGTATTTATTCAAAAC	657

Db 601 TCCTCTGGAGAGGCCCTGGCAGAACGAGAGGATGGGGACAGTATTATTCAAAC 657

RESULT 2
AAA73132
ID AAA73132 standard; cDNA; 1707 BP

AC AAA73132;

DT 27-NOV-2000 (first entry)

Human beta-transducin repeat containing protein (beta-TRCP) cDNA.

KM Ubiquitin ligase SCF complex; F-box protein; ubiquitination; IkappaB;
 KW beta-catenin; Skp1; Cull1; F-box motif; WD40 repeat motif; FMD1;
 KW gene therapy; colon cancer; beta-transducin repeat containing protein;
 KW beta-TICP; 85.

OS Homo sapiens.

PN JP2000166542-A.

PD 20-JUN-2000

PF 02-DEC-1998; 98JP-0343437.
VY

PR 02-DEC-1998; 98JP-0343437.
YY

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
YX

DR WPI; 2000-485550/43.
DB P-PSDB: AAF12813

F-box protein of
XX
PT

PI ubiquitination of IkappaB or beta-catenin -

PS Disclosure; Fig 1/; 19pp; Japanese.
XX

The present invention describes an F-box motif protein of ubiquitin ligase SCF complex which promotes the ubiquitination of IkappaB beta-catenin and is constituted by Sp1 protein, Cul1 protein and a co-receptor (SCF complex) of F-box protein containing F-box motif and repeat motif and has the amino acid sequence of 45 residues (AA312811) or one of two 569 residue sequences (AA312812, which is mouse ubiquitin ligase FMD1 protein) and (AA312813, which is human beta-transducin repeat containing protein (beta-TrCP)). The F-box protein can be used for the gene therapy of colon cancer by being recombined to a virus vector. The present sequence encodes the human beta-TrCP protein from the present invention.

SQ Sequence 1707 BP; 514 A; 349 C; 414 G; 430 T; 0 other;

Query Match	100.0%;	Score 657;	DB 21;	Length 1707;
-------------	---------	------------	--------	--------------

Best Local Similarity 100.0%; Pred. No. 1.9e-201;
Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches	657;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	----	--------	----	------	----

QY	1	ATGAGACCCGGCGAGGGCTGCTGCAGAAAGGACATCAAGTTATTAATTTCTCGAG	60
Db	1	ATGAGACCCGGCGAGGGCTGCTGCAGAAAGGACATCAAGTTATTAATTTCTCGAG	60
QY	61	AGAGAAAGACTGTATATATGGCGAACCCCTAGGAAGATATACGAGAGAAATTCATT	120
Db	61	AGAGAAAGACTGTATATATGGCGAACCCCTAGGAAGATATACGAGAGAAATTCATT	120
QY	121	AGACGACACTTACAAACAGCTGTGCCAGACTCTGCTTAAACCAGAAACGATTTGTTAGCA	180
Db	121	AGACGACACTTACAAACAGCTGTGCCAGACTCTGCTTAAACCAGAAACGATTTGTTAGCA	180
QY	181	AGCAGCTGCTATGAAGACTGAGAAATTGTGTGGCCAAACAAACCTTGGCAATGGCATTTCC	240
Db	181	AGCAGCTGCTATGAAGACTGAGAAATTGTGTGGCCAAACAAACCTTGGCAATGGCATTTCC	240
QY	241	AGTATGATTTGTGCCCAAGCAACGGAAGAACTCTTACGACGCTATGAAAAAGAAAAAGAACTG	300

Db 241 ACTATGATTGCCCCACCAACGAACTCTCAGCAAGATGAAAGAAAAGCAACTG 300
Oy 301 TGTGCAAACTACTTGTAGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 360
Db 301 TGTGCAAACTACTTGTAGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 360
Oy 361 ATATCCCAAAATGTGTATTTACCAACATGAGGACATTAATCTGTATCTTAACCTATGTTG 420
Db 361 ATATCCCAAAATGTGTATTTACCAACATGAGGACATTAATCTGTATCTTAACCTATGTTG 420
Oy 421 CAGAGAGATTTATTAATCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 480
Db 421 CAGAGAGATTTATTAATCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 480
Oy 481 CTGTCTATCTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 540
Db 481 CTGTCTATCTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 540
Oy 541 CGAGTGACCTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 600
Db 541 CGAGTGACCTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 600
Oy 601 TCTCTGTGAGAGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 657
Db 601 TCTCTGTGAGAGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 657

RESULT 3

AAx86501
ID AAx86501 standard; cDNA; 2151 BP.

AAx86501;

20-MAR-2003 (updated)
30-SEP-1999 (first entry)

cDNA encoding a human beta-transducin repeat containing protein.

Beta-transducin repeat containing protein; beta-Trcp; Skrip;
Kw proteosome degradation pathway; Vpu protein; beta-catenin;
Kw human immune deficiency virus-1; HIV-1; cellular protein; Ikappab;
Kw ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's;
Kw antiviral; antitumour; cell cycle regulation; protein degradation;
Kw and anti-inflammatory; osteo-articular inflammation; acute inflammation;
Kw tumour necrosis factor; ss.

Homo sapiens.

Key Location/Qualifiers
70..1779
CDS /tag= a
/product= beta-Trcp
/note= "beta-transducin repeat containing protein"

W09938969-A1.

05-AUG-1999.

29-JAN-1999; 99WO-PR00196.

09-DEC-1998; 98FR-0015545.
30-JAN-1998; 98FR-0001100.

(INSP) INST PASTEUR.
(INRM) INST NAT SANTE & RECH MEDICALE.

Arenzana Seisdedos F, Benarous R, Concordet J, Durand H;
Kroll M, Margotlin F;

WPI: 1999-469329/39.
P-PSDB: AAY24054.

PT New human beta-transducin repeat containing protein and its
PT fragments useful as, or to screen for, antiviral, antitumour,
PI anti-inflammatory and anti-Alzheimer's agents
PS
XX Claim 7: Page 57-60; 71pp: French.

CC The present sequence encodes a human beta-transducin repeat containing
CC protein (beta-Trcp). The protein directs proteins to the proteosome
CC degradation pathways. The protein is able to interact with the Vpu
CC protein of human immune deficiency virus-1 (HIV-1), cellular proteins
CC Ikappab or beta-catenin (bc) and/or protein Skrip. The protein controls
CC ubiquitinylation of phosphorylated proteins and thus their targeting to
CC proteosomes for degradation. Depending on whether the process is
CC inhibited or promoted, the result may be delayed breakdown of Cdk (in
CC cases of HIV-1 infection); increased activity of Ikb (and thus reduced
CC activity of NFkappab); increased degradation of mutant bc in tumour
CC cells, or increased bc survival (and reduced apoptosis) in Alzheimer's
CC patients. The beta-Trcp protein, and its active peptide fragments, or its
CC nucleic acid, are used to screen for anti HIV-1 agents (antivirals),
CC antitumour agents that disrupt cell cycle regulation or protein
CC degradation in human tumour cells, and anti-inflammatory agents that
CC disrupt activation by NFkappab. Fragments of the protein are also
CC useful for treating osteo-articular inflammation or acute inflammation
CC associated with release of tumour necrosis factor.
CC (Updated on 20-MAR-2003 to correct PA field.)
CC
XX

SQ Sequence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;

Query Match 100.0%; Score 657; DB 20; Length 2151;
Best local similarity 100.0%; Pred. No. 2,1e-201;
Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGACCCCGCCGAGCGGTGCTGCAAGAAAGCACTCAAGTTTATGATTCCTCAGAG 60
Db 70 ATGACCCCGCCGAGCGGTGCTGCTGCAAGAAAGCACTCAAGTTTATGATTCCTCAGAG 129
Oy 61 AGAAGAGCTGTATATATGCGCAACCCCTAGAGATATATACAGAGAAATTCACATT 120
Db 130 AGAAGAGCTGTATATATGCGCAACCCCTAGAGATATATACAGAGAAATTCACATT 189
Oy 121 AGACAGACATATACAGCTGTGCGACAGCTGTGTTAAACCAAGAAACATATATGAGA 180
Db 190 AGACAGACATATACAGCTGTGCGACAGCTGTGTTAAACCAAGAAACATATATGAGA 249
Oy 181 AGCACTGCTATGAGAGACTGAGATTTGTGGCCAAACAACTTCCATATGCACTTCC 240
Db 250 AGCACTGCTATGAGAGACTGAGATTTGTGGCCAAACAACTTCCATATGCACTTCC 309
Oy 241 AGTATGATTTGTGCCAAGCAAGCAAGAACTCTCAGCAAGCTATGAAAAAGAAAGACTG 300
Db 310 AGTATGATTTGTGCCAAGCAAGCAAGAACTCTCAGCAAGCTATGAAAAAGAAAGACTG 369
Oy 301 TGTGCAAACTACTTGTAGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 360
Db 370 TGTGCAAACTACTTGTAGCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 429
Oy 361 ATATCCCAATGTGTATTTACCAACATGAGGACATTAATCTGTATCTTAACCTATGTTG 420
Db 430 ATATCCCAATGTGTATTTACCAACATGAGGACATTAATCTGTATCTTAACCTATGTTG 489
Oy 421 CAGAGAGATTTATTAATCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 480
Db 490 CAGAGAGATTTATTAATCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 549
Oy 481 CTGTCTATCTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 540
Db 550 CTGTCTATCTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 609
Oy 541 CGAGTGACCTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 600
Db 610 CGAGTGACCTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 669
Oy 601 TCTCTGTGAGAGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 657

|||||
Db 670 TCTCTGTGGAGAGGCGCTGGCAGAACGAGAGATGGGAGCTATTATTTCACAAAC 726
RESULT 4
ID AAA51229 standard; DNA: 2151 BP.
XX
AC AAA51229;
XX
DT 26-SEP-2000 (first entry)
XX
DE Human beta-TrCP coding sequence.
XX
KW E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor;
KW nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;
KW anti-inflammatory; immunosuppressive; cytosolic; ds.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT CDS 70..1779
FT /*tag= a
FT /product= Human_TrCP
XX
PN MO200034447-A2.
XX
PD 15-JUN-2000.
XX
PF 10-DEC-1999; 99WO-US29371.
XX
PR 10-DEC-1998; 98US-0210060.
XX
PA (SIGN-) SIGNAL PHARM INC.
PA (YISS) YISSUM RES & DEV CO.
PI Manning AM, Mercurio F, Amit S, Ben-eriah Y, Davis M, Hatzubal A;
PI Layon I, Yaron A;
DR WPI: 2000-431294/37.
DR P-PSDB; NAY96697.
XX
XX Polypeptide enhancing phosphorylated I-kappaB ubiquitination useful for
PT treating disorder associated with NF-kappaB activation e.g. cancer,
PT comprising amino acid sequence of human E3 ubiquitin ligase or its
PT variant
XX
PS Disclosure; Page 72; 77pp; English.
XX
XX This DNA encodes human beta-TrCP, an F-box/WD protein family member,
CC which has been shown to have homology to human E3 ubiquitin ligase (E3).
CC E3 enhances ubiquitination of phosphorylated I-kappa-B, an inhibitor
CC protein of nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B
CC degradation via the ubiquitin pathway is useful for identifying
CC modulators of this process for use in treating diseases associated with
CC activation of NF-kappa-B. In vitro analysis suggests that deletion of
CC the F-box results in a protein that functions as a dominant negative
CC molecule in vivo. Transient over-expression of delta-beta-TrCP (a
CC deletion mutant) inhibited the degradation of endogenous I-kappa-B-alpha
CC in stimulated Jurkat cells, resulting in accumulation of phosphorylated
CC I-kappa-B-alpha. E3 can be used to screen for modulators of NF-kappa-B
CC activity. E3 and beta-TrCP can be used to modulate NF-kappa-B to treat
CC inflammatory diseases, autoimmune diseases, cancer and viral infections.
XX
SO Sequence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;
Query Match 100.0%; Score 657; DB 21; Length 2151;
Best Local Similarity 100.0%; Pred. No. 2.1e-201;
Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGACCCGCGGCGGCTGTCGCAAGAGAGCATCTCAAGTTTATGATTCTCTCAGAG 60
PR |||||||
Db 70 ATGAGACCCGCGGCGGCTGTCGCAAGAGAGCATCTCAAGTTTATGATTCTCTCAGAG 129

QY 61 AGAGAGACTGTATATATGCGGAACCCCTAGGAAGATTAATCCAGAGAGATTCTACTT 120
Db |||||||
QY 130 AGAGAGACTGTATATATGCGGAACCCCTAGGAAGATTAATCCAGAGAGATTCTACTT 189
QY 121 AGAGAGACTGTATATATGCGGAACCCCTAGGAAGATTAATCCAGAGAGATTCTACTT 180
Db |||||||
QY 190 AGAGAGACTGTATATATGCGGAACCCCTAGGAAGATTAATCCAGAGAGATTCTACTT 249
QY 181 AGAGAGACTGTATATATGCGGAACCCCTAGGAAGATTAATCCAGAGAGATTCTACTT 240
Db |||||||
QY 250 AGAGAGACTGTATATATGCGGAACCCCTAGGAAGATTAATCCAGAGAGATTCTACTT 309
QY 241 AGATGATTTGTCGCCAAGCAACGAACTCTCAGACACTTATGAAAGGAAAGGAACTG 300
Db |||||||
QY 310 AGATGATTTGTCGCCAAGCAACGAACTCTCAGACACTTATGAAAGGAAAGGAACTG 369
QY 301 TGTGCAATATCTTTGACAGTGGGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 360
Db |||||||
QY 370 TGTGCAATATCTTTGACAGTGGGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 429
Db |||||||
QY 361 ATATCCCAATATGTCATTTACCAACATGGGACATTAACCTGTAATCTTAACTATGTTG 420
Db |||||||
QY 430 ATATCCCAATATGTCATTTACCAACATGGGACATTAACCTGTAATCTTAACTATGTTG 489
QY 421 CAGAGAGATTTCATTAACGCTCTGCGACGCTGGGGATTTGATCATATGCTGAGAACATT 480
Db |||||||
QY 490 CAGAGAGATTTCATTAACGCTCTGCGACGCTGGGGATTTGATCATATGCTGAGAACATT 549
Db |||||||
QY 481 CTGTCAATACCTGATGCGCAATCACTATGTCCTCTGCAAGTCTGTCGAAGAAATGTCAC 540
Db |||||||
QY 550 CTGTCAATACCTGATGCGCAATCACTATGTCCTCTGCAAGTCTGTCGAAGAAATGTCAC 609
QY 541 CGAGTGAACCTGATGCGCAATCACTATGTCCTCTGCAAGTCTGTCGAAGAAATGTCAC 600
Db |||||||
QY 610 CGAGTGAACCTGATGCGCAATCACTATGTCCTCTGCAAGTCTGTCGAAGAAATGTCAC 669
QY 601 TCTCTGTGGAGAGGCGCTGGCAGAACGAGAGATGGGAGCTATTATTTCACAAAC 657
Db |||||||
Db 670 TCTCTGTGGAGAGGCGCTGGCAGAACGAGAGATGGGAGCTATTATTTCACAAAC 726
RESULT 5
ID AA293350 standard; cDNA: 2151 BP.
XX
XX AA293350;
XX
XX 16-AUG-2000 (first entry)
XX
XX Sequence encoding F-box protein FBP-1.
XX
XX F-box protein; FBP; diagnosis; treatment; screening; agonist;
XX antagonist; proliferative disorder; differential disorder;
XX breast cancer; prostate cancer; ovarian cancer; cancer;
XX small cell lung carcinoma; immune disorder; cardiovascular disorder;
XX inflammatory disorder; human; ss.
XX
XX Homo sapiens.
XX
XX
XX Key location/Qualifiers
XX CDS 70..1779
XX /*tag= a
XX /product= FBP-1
XX
XX MO200012679-A1.
XX
XX 09-MAR-2000.
XX
XX 27-AUG-1999; 99WO-US19560.
XX
XX 28-AUG-1998; 98US-0098355.
XX
XX 03-FEB-1999; 99US-0118568.
PR |||||||

PR 15-MAR-1999: 99US-0124449.
 XX (UWNY) UNIV NEW YORK STATE.
 XX
 PI Chlaur DS, Pagano M, Latres E;
 XX
 XX MPI: 2000-256635/22.
 DR F-PSDB; AA183041.
 XX
 XX Novel nucleic acid for screening compounds useful for treating
 PT proliferative and differentiative disorders such as cancer and immune
 PT disorders comprises sequences encoding ubiquitin ligases
 XX
 PS Disclousure; Figure 3b, 3c, 3d; 245pp; English.
 XX
 XX Nucleic acids encoding substrate-targeting subunits of ubiquitin
 CC ligases with F-box motifs (F-box proteins) are useful for diagnosis
 CC of proliferative and differentiated related disorders by measuring
 CC FBP gene expression. Cells expressing such proteins or
 CC their fragments are useful for screening compounds. The compounds
 CC are agonists or antagonists, which are useful for treating a
 CC proliferative or differentiative disorder in a mammal such as
 CC breast, ovarian and prostate cancer and small cell lung carcinoma
 CC and also major opportunistic infections, immune disorders,
 CC cardiovascular diseases and inflammatory disorders. FBP protein,
 CC analogs, derivatives and their subsequences, anti-FBP antibodies,
 CC are also useful in diagnosis of the disorders.
 XX

Sequence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;

Query Match 100.0%; Score 657; DB 21; Length 2151;
 Best Local Similarity 100.0%; Pred. No. 2.1e-201;
 Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGGACCCGGCGGAGGCGTGCAGAGAGGCGACATGTTATGATTCCTCAGAG 60
 DB 70 ATGGACCCGGCGGAGGCGTGCAGAGAGGCGACATGTTATGATTCCTCAGAG 129
 OY 61 AGAGAGACTGTAATTAATGCGCAACCCCTAGAGATTAATACAGAGAGAAATTCATT 120
 DB 130 AGAGAGACTGTAATTAATGCGCAACCCCTAGAGATTAATACAGAGAGAAATTCATT 189
 OY 121 AGACAGACTATACAGAGCTGTGCGACAGCTCTGCTTAACCCAGAAAGAACTATGTTAGCA 180
 DB 190 AGACAGACTATACAGAGCTGTGCGACAGCTCTGCTTAACCCAGAAAGAACTATGTTAGCA 249
 OY 181 AGCAGCTGTATGAAGCTGAGAAATTTGTGGCCAAAGAACTTCCCAATGGCACTTCC 240
 DB 250 AGCAGCTGTATGAAGCTGAGAAATTTGTGGCCAAAGAACTTCCCAATGGCACTTCC 309
 OY 241 AGTATGATTTGTCGCCAAGCAGAACTCTCAGCAAGCTATGAAAAAGAAAGAACTG 300
 DB 310 AGTATGATTTGTCGCCAAGCAGAACTCTCAGCAAGCTATGAAAAAGAAAGAACTG 369
 OY 301 TGTGTCAATTAATTTGAGCAGTGTGAGTCAAGTCAAGTGAATTTTGTGAACATCTT 360
 DB 370 TGTGTCAATTAATTTGAGCAGTGTGAGTCAAGTCAAGTGAATTTTGTGAACATCTT 429
 OY 361 AATATCCCAATGTCATTAACCAACATGGGCATTAATGCAATGTTAACTTAAGTTG 420
 DB 430 AATATCCCAATGTCATTAACCAACATGGGCATTAATGCAATGTTAACTTAAGTTG 489
 OY 421 CAGAGAGATTTTCAATTAATGCTCTGCCAGCTCGGGGATTTGATCAATATCCCTGAGAACAT 480
 DB 490 CAGAGAGATTTTCAATTAATGCTCTGCCAGCTCGGGGATTTGATCAATATCCCTGAGAACAT 549
 OY 481 CTGTCTATCTGATGAGCCCAATCACTATGCTGCTGAACCTGTGTGCAAGAAAGTAC 540
 DB 550 CTGTCTATCTGATGAGCCCAATCACTATGCTGCTGAACCTGTGTGCAAGAAAGTAC 609
 OY 541 CGAGTGACCTGTGATGGCATGCTGCGAAGCAAGCTTATGAGAGATTTGTCAGGACAGAT 600
 DB 610 CGAGTGACCTGTGATGGCATGCTGCGAAGCAAGCTTATGAGAGATTTGTCAGGACAGAT 669

OY 601 TCTCTGTGAGAGGCTGCGACAGAACAGAGATGGGACAGTATTATTCAAAAC 657
 DB 670 TCTCTGTGAGAGGCTGCGACAGAACAGAGATGGGACAGTATTATTCAAAAC 726

RESULT 6
 AA293710
 ID AA293710 standard; DNA; 2151 BP.
 XX
 AC AA293710;

DE 16-AUG-2000 (first entry)

DE F-box protein hbetaTrcP coding sequence.

KW Ubiquitin ligase; SCF; F-box protein; targeted degradation;
 KW destabilisation; proteolysis; drug discovery; gene therapy; cancer;
 KW oncoprotein; Huntington's disease; gene knockout; delivery systems;
 KW human; ss.

OS Homo sapiens.

EH Key Location/Qualifiers

FT CDS 70..179
 FT /tag- a
 FT /product- F-box protein hbetaTrcP

PN MO200022110-A2.

XX 20-APR-2000.

PD 08-OCT-1999; 99NO-US23705.

PR 09-OCT-1998; 98US-0103787.

PA (HARD) HARVARD COLLEGE.

PI Zhou P, Howley P;

DR MPI: 2000-317970/27.

PS P-PSDB; AA183250.

PT Targeting degradation of polypeptide useful for treating cancer and
 PT other proliferative disorders, involves conjugating polypeptide with
 PT ubiquitin protein ligase or inhibiting ubiquitination using organic
 PT compound

PS Claim 10; Page 171; 185pp; English.

XX The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin
 CC ligases) which can be used for the targeted degradation of a target
 CC polypeptide in vivo. Targeted degradation is achieved by expressing
 CC the ubiquitin ligase in a cell linked to the interaction domain of
 CC the target polypeptide and thereby recruiting the target polypeptide
 CC to the ubiquitin ligase. Such methods are useful for decreasing or
 CC increasing the level of a target polypeptide and for creating and
 CC expressing a destabilized polypeptide which is subjected to SCF
 CC mediated proteolysis. Degrading any desired protein in a cell is
 CC useful for preventing or treating diseases caused by the presence of
 CC abnormal amount of the specific polypeptides, for drug discovery and
 CC for gene therapy. Diseases treated include cancer, by degradation of
 CC oncoproteins, Huntington's disease, other proliferative disorders and
 CC microbial infections. The method provides a quick and easy
 CC alternative to gene knockout technology. The target polypeptide can
 CC be degraded at all stages, or a specific stage, of development in the
 CC mature animal.

Sequence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;

Query Match 100.0%; Score 657; DB 21; Length 2151;
 Best Local Similarity 100.0%; Pred. No. 2.1e-201;
 Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGAGCCCGGCGGAGCGGTGCTGCAAGAGAAAGGACATCAAGTTATGAAATTCCTCGAG	60
Db	70	ATGAGACCCGCGGAGCGGTGCTGCGAAGAGAAAGGACATCAAGTTATGAAATTCCTCGAG	125
QY	61	AGAGAAAGACTGTAAATTAATGGCGAACCCCTAGGAAGATTAATCCAGAGAAATTCACTT	120
Db	130	AGAGAAAGACTGTAAATTAATGGCGAACCCCTAGGAAGATTAATCCAGAGAAATTCACTT	185
QY	121	AGACACACATACAAACAGCTGTGCCAGACTCTGTCTTAAACCAAGAAACAGTATGTTTAGCA	180
Db	190	AGACACACATACAAACAGCTGTGCCAGACTCTGTCTTAAACCAAGAAACAGTATGTTTAGCA	245
QY	181	AGACACTGTATGAAAGACTGAGAATTTGTGTGGCCAAACAAACCTTGGCAATGGCACTTCC	240
Db	250	AGACACTGTATGAAAGACTGAGAATTTGTGTGGCCAAACAAACCTTGGCAATGGCACTTCC	305
QY	241	AGTATGATTTGTGTGCCAGACGAAACTCTCAGCAAGCTATGAAAAGAAAAGAACTG	300
Db	310	AGTATGATTTGTGTGCCAGACGAAACTCTCAGCAAGCTATGAAAAGAAAAGAACTG	365
QY	301	TGTGTAAATTAATTTGAGCAGTGTGTCAGAGTCAGATCAAGTGAATTTGTGGAACATCTT	360
Db	370	TGTGTAAATTAATTTGAGCAGTGTGTCAGAGTCAGATCAAGTGAATTTGTGGAACATCTT	425
QY	361	ATATCCCAATGTGTCTATTACCAACATGCGGCACATAACTGGTATCTTAAACGTATGTG	420
Db	430	ATATCCCAATGTGTCTATTACCAACATGCGGCACATAACTGGTATCTTAAACGTATGTG	485
QY	421	CAGAAGATTTTCATTAACCTCTCTGCCAGCTCGGGGATTGGATCATATGCTGAGAACATT	480
Db	490	CAGAAGATTTTCATTAACCTCTCTGCCAGCTCGGGGATTGGATCATATGCTGAGAACATT	545
QY	481	CTGTCAATACCTGGATGCCAAATCACTATGTGCTGTAACCTTGTGTGCAAGGAATGGTAC	540
Db	550	CTGTCAATACCTGGATGCCAAATCACTATGTGCTGTAACCTTGTGTGCAAGGAATGGTAC	605
QY	541	CGAGTAGCCTCTGATGGATGCTGTGGAGAAAGCTTATCGAGAGAAATGGTCAGACAGAT	600
Db	610	CGAGTAGCCTCTGATGGATGCTGTGGAGAAAGCTTATCGAGAGAAATGGTCAGACAGAT	665
QY	601	TCCTCTGTGAGAGGCGCTGGCAACAAGAAAGATGGGACAGTATTATTCAAAAAC	657
Db	670	TCCTCTGTGAGAGGCGCTGGCAACAAGAAAGATGGGACAGTATTATTCAAAAAC	726
RESULT 7			
AAC84610			
ID	AAC84610 standard: DNA; 2151 BP.		
XX	AAC84610;		
AC	AAC84610;		
XX	AAC84610;		
DT	02-Apr-2001 (first entry)		
XX	Human ZF11 protein encoding DNA.		
DE	Human ZF11 protein encoding DNA.		
XX	S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;		
KW	CUL-1; cullin; CD53; p27; cyclin E; Max; Med; c-Myc; MDM2; p53; Bax;		
KW	Bad; Bcl-2; tumour; cytosolic; ds.		
OS	Homo sapiens.		
XX	MO200075184-A1.		
PN	14-DEC-2000.		
PD	14-DEC-2000.		
XX	05-JUN-2000; 2000MO-US15449.		
PF	05-JUN-2000; 2000MO-US15449.		
XX	04-JUN-1999; 99US-0137494.		
PR	04-JUN-1999; 99US-0137494.		
XX	(UYIA) UNIV YALE.		
PA	(UYIA) UNIV YALE.		
XX	Zhang H, Tsvelkov LM, Kondo T;		
PI	Zhang H, Tsvelkov LM, Kondo T;		

XX	WPI: 2001-061703/07.
DR	P-PSDB; AAB48298.
XX	
PT	Modulating polypeptide levels in a cell, diagnosing and treating tumor,
PT	involves altering levels of proteins such as S-phase kinase associated
PT	proteins 1, 2 and cullin/CDC5 proteins -
XX	
XX	Examples: Page 129-130; 162pp; English.
CC	The invention relates to methods of altering the polypeptide levels in a
CC	cell, using proteins selected from S-phase kinase associated proteins 1
CC	and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
CC	cullin/CDC5 family of proteins). The method is useful for altering the
CC	level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
CC	polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
CC	detecting tumours, and in monitoring tumor treatment in a mammal. Agents
CC	treat modulate interactions between Skp and target proteins are useful for
CC	treating tumors.
XX	
SQ	Sequence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;
	Query Match 100.0%; Score 657; DB 22; Length 2151;
	Best Local Similarity 100.0%; Pred. No. 2.1e-201;
	Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 ATGGACCGGCGCGAGCGGTCTGCAGAAGAACGACTCAAGTTATGAATTCCTCAGAG 60
Dd	70 ATGGAACCGCGCGAGCGGTCTGCAGAAGAACGACTCAAGTTATGAATTCCTCAGAG 129
QY	61 AGAAGAACTTAATAATGGGGAACCCCTTGGAAATATTACCAGAGAAATTCCT 120
Dd	130 AGAAGAACTTAATAATGGGGAACCCCTTGGAAATATTACCAGAGAAATTCCT 189
QY	121 AGACAGACATACAACAGCTGTGCCAGACTTGCTTAACCAAAGAACAGTAGTTAGCA 180
Dd	190 AGACAGACATACAACAGCTGTGCCAGACTTGCTTAACCAAAGAACAGTAGTTAGCA 249
QY	181 AGCACTGCTATGAAGACTGAGAAATTTGTGTGGCCAAAACAACTTCCCATGGCACTTCC 240
Dd	250 AGCACTGCTATGAAGACTGAGAAATTTGTGTGGCCAAAACAACTTCCCATGGCACTTCC 309
QY	241 AGTATGATTTGGCCCAACGAAAGAACTTCAGCAAGCTATGAAAAAGAAAGAACG 300
Dd	310 AGTATGATTTGGCCCAACGAAAGAACTTCAGCAAGCTATGAAAAAGAAAGAACG 369
QY	301 TGTTGCAATCTTTGAGCAGTAGTGTGACAGTCAGATCAAGTGAATTTGTGGACATCTT 360
Dd	370 TGTTGCAATCTTTGAGCAGTAGTGTGACAGTCAGATCAAGTGAATTTGTGGACATCTT 429
QY	361 ATTATCCCAATNGTGTCAATTACCAACATGGGCATATAACTGTATTTAACTTATGTTG 420
Dd	430 ATTATCCCAATNGTGTCAATTACCAACATGGGCATATAACTGTATTTAACTTATGTTG 489
QY	421 CAGAGAGATTTTCATTAAGTCTGTGGCACCTGGGGATTTGGATCATATGGCTGAGAACAT 480
Dd	490 CAGAGAGATTTTCATTAAGTCTGTGGCACCTGGGGATTTGGATCATATGGCTGAGAACAT 549
QY	481 CTGTCAATACCTGGATGCCAAATCACTATGTCTGTGAACCTTGTGCAAGGAATGGTAC 540
Dd	550 CTGTCAATACCTGGATGCCAAATCACTATGTCTGTGAACCTTGTGCAAGGAATGGTAC 609
QY	541 CGAATGAACTCTGATGGCATGCTGTGGAAAGACTTATTCGAGAGAAATGGTCAAGACAGAT 600
Dd	610 CGAATGAACTCTGATGGCATGCTGTGGAAAGACTTATTCGAGAGAAATGGTCAAGACAGAT 669
QY	601 TCTCTGTGGAAGAGCTGGCAGAAAGAGAGATGGGACAGTATTTATCAAAAAC 657
Dd	670 TCTCTGTGGAAGAGCTGGCAGAAAGAGAGATGGGACAGTATTTATCAAAAAC 726

ID	AL41041 standard; CDNA; 2151 BP.
XX	
AC	AL41041;
XX	
DT	11-OCT-2002 (first entry)
XX	
DE	CDNA of Human F-box protein FBP1 SEQ ID NO 1.
XX	
KW	Cytostatic; immunomodulator; cardiac; antiinflammatory; antimicrobial;
KW	proliferative; differentiative disorder; Skp2; F-box protein; cancer;
KW	ubiquitin ligase; breast cancer; prostate cancer; ovarian cancer;
KW	small cell lung carcinoma; immune disorder; parathyroid adenoma; FBP;
KW	inflammatory disorder; lymphoma; major opportunistic infection;
KW	certain cardiovascular disease; human; gene; ss.
XX	

OS Homo sapiens.
XX
PN W0200255665-A2.
XX
PD 18-JUL-2002.
XX
PF 07-JAN-2002; 2002WO-US00311.
XX
PR 05-JAN-2001; 2001US-260179P.
XX
PA (UINY) UNIV NEW YORK STATE.

PI Pagano M;
XX
DR WPI: 2002-599665/64.
DR P-PSDB: AAO22446.

PT Screened compounds for treating proliferative disorders, e.g. breast
 PT cancer or prostate cancer, infections or immune disorders, comprises
 PT detecting a change in the activity of Skp2 with either p27 or Cks1 -
 XX
 XX
 XX Disclosure; Fig 3; 246pp; English.

CC The invention relates to screening compounds useful for the treatment of
CC proliferative or differentiative disorders comprising detecting a change
CC in the activity of Shp2 (F-box protein). The method is useful for
CC screening compounds for the treatment of proliferative or differentiative
CC disorders, particularly cancer. These compounds include small molecules,
CC or compounds or derivatives or analogues of the new ubiquitin ligases.
CC The compounds are useful for treating diseases such as cancer (e.g.
CC breast cancer, prostate cancer or ovarian cancer, lymphoma, small cell
CC lung carcinoma or parathyroid adenomas), major opportunistic infections,
CC immune disorders, certain cardiovascular diseases or inflammatory
CC disorders. This polynucleotide sequence represents the cDNA encoding an
CC F-box protein (FBP) of the invention.

SQ Sequence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other,

Query Match	100.0%	Score 657;	DB 24	Length 2151;
Best Local Similarity	100.0%	Pred. No. 2.1e-201;		
Matches 657; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 ATGAGACCCGGCCGAGCGCGTGCTGCTCCAGAGAGAGGCACTCAAGTTTATGAATTTCTCAGAG 60
Db 70 ATGAGACCCGGCCGAGCGCGTGCTGCTCCAGAGAGAGGCACTCAAGTTTATGAATTTCTCAGAG 129

OY 61 AGAGNAGACTGTATTAATGCGCAACCCCTAGGAAGATATACCAGAGAAGAAATTCACTT 120
|||||
|||||
Db 130 AGGAGAGACTGTATAATGGCGAACCCCTAGGAAGATATACCAGAGAAGAAATTCACTT 189
|||||
|||||

QY 121 AGACAGACATCAACAACGCTGTGCCAGACTCTGCCTTAACCAGAAGAACAGTATGTTTAGCA 180
Db 190 AGCAGACAGCTTACAACAGCTGTGCCAGACTCTGCCTTAACCAGAAGAACAGTATGTTTAGCA 249	

Qy 181 AGCACTGCTATGAAAGACTGAGAAATTTGTGTGGCCAAAACAAACCTTGGCAATGGCACTTCC 240
 |||||
 Db 250 AGCACTGCTATGAAAGACTGAGAAATTTGTGTGGCCAAAACAAACCTTGGCAATGGCACTTCC 309
 |||||

OY	241	AGTAGATGTTGGCCCAAGCAACGGAAACCTCAGCAAGCTATGAAANAGAAAGAAACCTG	3000
Db	310	AGTAGATGTTGGCCCAAGCAACGGAAACCTCAGCAAGCTATGAAANAGAAAGAAACCTG	3659
OY	301	TGTGTCAAAATACCTTTGAGCAGTGTGTGCAGAGTCAGATCAAGTGGAAATTTGTGGAAACATCTT	3605
Db	370	TGTGTCAAAATACCTTTGAGCAGTGTGTGCAGAGTCAGATCAAGTGGAAATTTGTGGAAACATCTT	4299
OY	361	ATATCCCAAAATGTGTTCATTACCAACATGGGCAATTAACCTGATCTTAAACCTATGTTG	4200
Db	430	ATATCCCAAAATGTGTTCATTACCAACATGGGCAATTAACCTGATCTTAAACCTATGTTG	4894
OY	421	CAGAGAGATTTTCATTAACCTGTCTGCGCAGCTCGGGGATTTGGATTCATATCGCTGGAAACATT	4800
Db	490	CAGAGAGATTTTCATTAACCTGTCTGCGCAGCTCGGGGATTTGGATTCATATCGCTGGAAACATT	5494
OY	481	CTGTATACCTTGGATGGCCAAATCACATATGTGCTGTGCAACTGTGTGCAAGAGAAATGGTAC	5400
Db	550	CTGTATACCTTGGATGGCCAAATCACATATGTGCTGTGCAACTGTGTGCAAGAGAAATGGTAC	6099
OY	541	CGAGTGACCTCTGATGGCATGTGCTGTGGAAGAAACCTTATCGAGAGAAATGGTCACGACAGAT	6000
Db	610	CGAGTGACCTCTGATGGCATGTGCTGTGGAAGAAACCTTATCGAGAGAAATGGTCACGACAGAT	6659
OY	601	TCTCTGTGGAGGGCTGGCGACAACGAAGAAGATGGGGACAGATTTATTTCAAAAAC	657
Db	670	TCTCTGTGGAGGGCTGGCGACAACGAAGAAGATGGGGACAGATTTATTTCAAAAAC	726

```

RESULT 9
ABS51009
ID ABS51009 standard; cDNA; 2151 BP

```

AC	ABS51009;
XX	
DT	21-OCT-2002 (first entry)
DT	

DE Human cDNA encoding bait protein beta-TrCP1.

KM Human; ss; gene; yeast two-hybrid assay; adipocyte; bait protein; NIDDM;
 KM non-insulin diabetes mellitus; obesity; selected interacting domain;
 KM SID; protein-protein interaction map; PIM; anorectic; metabolic disorder.
 XX
 OS Homo sapiens.

PN W0200253726-A2.

PD 11-JUL-2002.

PF 28-DEC-2001; 2001WO-EP15423.

PR 02-JAN-2001; 2001US-259377P.

PA (HYBR-) HYBRIGENICS.

XX

XX

DR P-PSDB; ABG69473.

PT Novel complex of pro

PT and useful for treat

PS Claim 2; Page -; 125pp; English.

CC The invention relates to a complex of protein-protein interactions
CC (forming a protein-protein interaction map, PIM) in adipocyte cells as
CC defined in the specification, or polynucleotides in adipocytes encoding
CC for the polypeptides. Also included are a recombinant cell expressing the
CC interacting polypeptides and a method of selecting a modulating compound
CC in adipocyte cells, by cultivating a recombinant host cell on a selective

CC medium containing a modulating compound and a reporter gene the
 CC expression of which is toxic for the recombinant host cell which is
 CC transformed with two vectors, where the first vector comprises a
 CC polynucleotide encoding a first hybrid polypeptide and DNA binding
 CC domain and the second vector comprising a polynucleotide encoding a
 CC second hybrid polypeptide and an activating domain that activates the
 CC toxic reporter gene, when the first and second hybrid polypeptides
 CC interact and selecting the modulating compound which inhibits the
 CC growth of the recombinant host cell (i.e. using the yeast two-hybrid
 CC system). The complexes are useful for identifying compounds that modulate
 CC the protein-protein interactions and useful for treating obesity and
 CC metabolic disorders e.g. non-insulin dependent diabetes mellitus,
 CC NIDDM. The compound isolated by the method is useful for treating and
 CC preventing obesity or metabolic diseases. The interactions between
 CC the proteins of the complex further define a set of selected interacting
 CC domains, SID. The present sequence encodes a member of the protein
 CC complex of the invention, used as the bait protein in the yeast two-
 CC hybrid assay.
 CC Note: The present sequence was not displayed in the specification but
 CC was obtained from its Genbank entry by the indexer.
 CC
 XX
 XX Sequence 2151 BP: 628 A: 467 C: 513 G: 543 T: 0 other;

Query Match 100.0%; Score 657; DB 24; Length 2151;
 Best Local Similarity 100.0%; Pred. No. 2,1e-201;
 Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGACCCGGCGGCGGTGCTGCAAGAGAGGAGCTCAAGTTATGAAATTCCTCAGAG 60
 DB 70 ATGAGACCCGGCGGCGGTGCTGCTCAAGAGAGGAGCTCAAGTTATGAAATTCCTCAGAG 129
 QY 61 AGAGAAAGCTGTATATATGCGGAACCCCTTAGAAGATTAATCCAGAGAGAAATTCCT 120
 DB 130 AGAGAAAGCTGTATATATGCGGAACCCCTTAGAAGATTAATCCAGAGAGAAATTCCT 189
 QY 121 AGACAGACATACACAGCTGTGCGGAGCTGCTTAAACCAAGAAAGATGTTTGA 180
 DB 190 AGACAGACATACACAGCTGTGCGGAGCTGCTTAAACCAAGAAAGATGTTTGA 249
 QY 181 AGCAGCTGTATGAGAGCTGAGAAATGTGTGCGCAAAACAAACTTGGCAATGACCTTCC 240
 DB 250 AGCAGCTGTATGAGAGCTGAGAAATGTGTGCGCAAAACAAACTTGGCAATGACCTTCC 309
 QY 241 AGATATGATTTGTCGCCCAAGCAAGCAAACTCTACCAAGCTTGAAGAAAGAAAGAACTG 300
 DB 310 AGATATGATTTGTCGCCCAAGCAAGCAAACTCTACCAAGCTTGAAGAAAGAAAGAACTG 369
 QY 301 TGTGTCAAAATCTTTGAGCAGTGTGAGAGTCAGATCAAGTGAATTTGTGGAACATCTT 360
 DB 370 TGTGTCAAAATCTTTGAGCAGTGTGAGAGTCAGATCAAGTGAATTTGTGGAACATCTT 429
 QY 361 ATATCCCAATGTGTCTATTACCAATGAGGACATAAATCTGTATTTAAACCTATGTTG 420
 DB 430 ATATCCCAATGTGTCTATTACCAATGAGGACATAAATCTGTATTTAAACCTATGTTG 489
 QY 421 CAGAGAGATTTCAATTAATGCTGTGCGCAGCTCGGGGATTTGATCATCGCTGAGAAAT 480
 DB 490 CAGAGAGATTTCAATTAATGCTGTGCGCAGCTCGGGGATTTGATCATCGCTGAGAAAT 549
 QY 481 CTGTCAATACCTGTGATGCCAATCAATCAATGTGTGCTGCTGAATTTGTGCAAGATGTTAC 540
 DB 550 CTGTCAATACCTGTGATGCCAATCAATCAATGTGTGCTGCTGAATTTGTGCAAGATGTTAC 609
 QY 541 CGAGTGACCTGTGATGCGATGCTGTGGAAGAAGCTTATGAGAGAAATGTCAGAGACAT 600
 DB 610 CGAGTGACCTGTGATGCGATGCTGTGGAAGAAGCTTATGAGAGAAATGTCAGAGACAT 669
 QY 601 TCTCTGTGAGAGGCGCTGCGAGAAAGAGAGATGGGAGACATTTATTTCAAAAC 657
 DB 670 TCTCTGTGAGAGGCGCTGCGAGAAAGAGAGATGGGAGACATTTATTTCAAAAC 726

RESULT 10

AA229233
 ID AA229233 standard; cDNA; 2419 BP.
 AC AA229233;
 XX
 DT 28-FEB-2000 (first entry)
 XX
 DE Human cell signalling protein-12 encoding cDNA.
 XX
 KW Cell signalling protein-12; CSIGP-12; cell proliferation;
 KW inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS;
 KW arteriosclerosis; Addison's disease; multiple sclerosis; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 70..1779
 FT /tag=a
 FT /product="Cell Signalling Protein-12"
 FT
 XX
 PN WO958558-A2.
 XX
 PD 18-NOV-1999.
 XX
 PE 13-MAY-1999; 99WO-US10567.
 XX
 PR 13-MAY-1998; 98US-0085343.
 PR 26-AUG-1998; 98US-0098010.
 XX
 PA (INCYTE) INCYTE PHARM INC.
 XX
 PI Bandman O, Hillman JL, Lal P, Yue H, Tang, YT, Patterson C;
 PI Baughn MR, Yang J;
 XX
 DR MPI: 2000-086432/07.
 DR P-PSDB: AAY44249.
 XX
 PT Human cell signalling proteins useful for, e.g. diagnosing cell
 PT proliferative and inflammatory disorders
 PT
 PS Claim 9; Page 87-88; 90pp; English.
 XX
 CC The present sequence is a cDNA obtained from Incyte clone 3239149 of
 CC COLAUCT01 library. It encodes cell signalling protein-12 (CSIGP-12). It
 CC is expressed in musculo-skeletal, gastrointestinal and nervous
 CC tissues. Fragments of CSIGP encoding nucleic acid can be used as
 CC hybridisation probe for detecting CSIGP related sequences or allelic
 CC variants. Recombinant CSIGP can be produced in host cells by transforming
 CC them with genetically engineered vectors. Agonists or antagonists can be
 CC used in the treatment of cell proliferative and inflammatory disorders
 CC associated with decreased or increased CSIGP expression. CSIGP is used in
 CC the diagnosis, prevention and treatment of cell proliferative disorders
 CC like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory
 CC disorders like AIDS, Addison's disease, multiple sclerosis, etc.
 CC
 XX
 SO Sequence 2419 BP: 671 A: 531 C: 625 G: 590 T: 2 other;

Query Match 99.8%; Score 655.4; DB 21; Length 2419;
 Best Local Similarity 99.8%; Pred. No. 7.3e-201;
 Matches 656; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGACCCGGCGGCGGTGCTGCAAGAGAGGAGCTCAAGTTATGAAATTCCTCAGAG 60
 DB 70 ATGAGACCCGGCGGCGGTGCTGCTCAAGAGAGGAGCTCAAGTTATGAAATTCCTCAGAG 129
 QY 61 AGAGAAAGCTGTATATATGCGGAACCCCTTAGAAGATTAATCCAGAGAGAAATTCCT 120
 DB 130 AGAGAAAGCTGTATATATGCGGAACCCCTTAGAAGATTAATCCAGAGAGAAATTCCT 189
 QY 121 AGACAGACATACACAGCTGTGCGGAGCTGCTTAAACCAAGAAAGATGTTTGA 180
 DB 190 AGACAGACATACACAGCTGTGCGGAGCTGCTTAAACCAAGAAAGATGTTTGA 249


```

OY 181 AGCACTGCTATGAGACACTGAGAAATTTGTGTGGCCAAAACAACTTGCCATGTGCACCTTC 240
DB 230 AGCACTGCTATGAGAACTGAGAAATTTGTGTGGCCAAAACAACTTGCCATGTGCACCTTC 309
OY 241 AGTATGATTTGGCCCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 300
DB 310 AGTATGATTTGGCCCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 369
OY 301 TGTGTCAAAATCTTTGAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 370 TGTGTCAAAATCTTTGAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 429
OY 361 ATATCCCAAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 430 ATATCCCAAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 489
OY 421 CAGAGAGATTTCAATCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
DB 490 CAGAGAGATTTCAATCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 549
OY 481 CTGTCTATCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
DB 550 CTGTCTATCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 609
OY 541 CGAGTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB 610 CGAGTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 669
OY 601 TCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 657
DB 670 TCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 726

```

RESULT 11

AAH90079 standard; cDNA; 3220 BP.

AAH90079;

01-OCT-2001 (first entry)

Human bone marrow cDNA, SEQ ID NO: 323.

Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;

antiviral; antibacterial; antifungal; anti-HIV; haemostatic;

immunosuppressive; gene therapy; cytokine cell proliferation;

cell differentiation modulator; immune disorder; infection; cancer;

human immunodeficiency virus; HIV; autoimmune disorder; haemophilia; ss.

Homo sapiens.

WO200153453-A2.

26-JUL-2001.

23-DEC-2000; 2000WO-US34960.

21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0631450.

14-SEP-2000; 2000US-0662191.

19-OCT-2000; 2000US-0693036.

30-NOV-2000; 2000US-0250583.

(HYSE-) HYSEQ INC.

```

DR P-PSDB; AAM00960.
XX
PT Novel bone-marrow-expressed polynucleotides and polypeptides, useful
PT for treating e.g. cancer and immune deficiency disorders -
XX
PS Claim 1; Page 428; 648pp; English.
XX
CC The present sequence is one of 251 novel human polynucleotides
CC expressed in the bone marrow. The polynucleotide and the
CC polypeptide encoded by it are useful in the treatment of various
CC immune deficiencies and disorders. The deficiencies and disorders may
CC be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal
CC infection, or may result from an autoimmune disorder, a coagulation
CC disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
CC suppression of an inflammatory response or treatment of a nervous
CC system disorder such as Alzheimer's disease. Detection of the presence
CC or increased expression of the polynucleotide or the protein it
CC encodes is useful for the diagnosis and/or prognosis of one
CC or more types of cancer. The polynucleotide and polypeptide can be
CC used as nutritional sources or supplements and in the screening of
CC chemical compounds as potential drugs.
XX
SQ Sequence 3220 BP; 878 A; 725 C; 770 G; 847 T; 0 other;

```

```

Query Match 99.3%; Score 652.2; DB 22; Length 3220;
Best Local Similarity 99.5%; Pred. No. 9, 1e-200;
Matches 654; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

OY 1 ATGGACCCCGGCGGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 60
DB 128 ATGGACCCCGGCGGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 187
OY 61 AGAGAAAGCTGTAAATATGCGCAACCCCTAGAGATTAATACAGAGAAATTCACCTT 120
DB 188 AGAGAAAGCTGTAAATATGCGCAACCCCTAGAGATTAATACAGAGAAATTCACCTT 247
OY 121 AGACAGACATACACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
DB 248 AGACAGACATACACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 307
OY 181 AGCACTGCTATGAGACACTGAGAAATTTGTGTGGCCAAAACAACTTGCCAAATGGCACTTCC 240
DB 308 AGCACTGCTATGAGACACTGAGAAATTTGTGTGGCCAAAACAACTTGCCAAATGGCACTTCC 367
OY 241 AGTATGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
DB 368 AGTATGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 427
OY 301 TGTGTCAAAATCTTTGAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 428 TGTGTCAAAATCTTTGAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 487
OY 361 ATATCCCAAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 488 ATATCCCAAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 547
OY 421 CAGAGAGATTTCAATCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
DB 548 CAGAGAGATTTCAATCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 607
OY 481 CTGTCTATCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
DB 608 CTGTCTATCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 667
OY 541 CGAGTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB 668 CGAGTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 727
OY 601 TCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 657
DB 728 TCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 784

```

WPI: 2001-488707/53.

```
RESULT 12
AAK51715
ID AAK51715 standard; cDNA; 2285 BP.
XX
XX AAK51715;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 260.
XX
XX Human cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukemia;
XX nervous system disorder; arthritis; inflammation; ss.
XX
XX Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US04098.
XX
XX 03-FEB-2000; 2000US-0496914.
XX 27-APR-2000; 2000US-0560875.
XX 20-JUN-2000; 2000US-0598075.
XX 19-JUL-2000; 2000US-0620325.
XX 01-SEP-2000; 2000US-0654936.
XX 15-SEP-2000; 2000US-0663561.
XX 20-OCT-2000; 2000US-0693325.
XX 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Dimaac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
XX Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wehrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
XX P-PsDB; AAM78582.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX useful in diagnosis and gene therapy -
XX
XX Claim 1; Page 1177-1180; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, hematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukemia, nervous system disorders, arthritis and
XX inflammation.
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX (AAM80020) are omitted as the relevant pages from the sequence listing
XX were missing at the time of publication.
XX
XX Sequence 2285 BP; 646 A; 492 C; 573 G; 574 T; 0 other;
XX
XX Query Match 92.9%; Score 610.2; DB 22; Length 2285;
XX Best Local Similarity 99.5%; Pred. No. 2.9e-186;
XX Matches 612; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 43 TTTATGAAATTCCTAGAGAGAGAAAGACTGTAATATGCGCAACCCCTAGAGATATA 102
XX TTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
XX 277 TTATGTAATTCCTAGAGAGAGAAAGACTGTAATATGCGCAACCCCTAGAGATATA 336
XX
XX 103 CCAGAGAAAGAAATTCCTAGAGAGAGAAAGACTGTAATATGCGCAACCCCTAGAGATATA 162
XX TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
XX
```

```
DB 337 CCAGAGAAAGAAATTCCTAGAGAGAGAAAGACTGTAATATGCGCAACCCCTAGAGATATA 396
XX
XX 163 GAAACAGTATGTTTATAGCAAGCAGTGTATGAAGACTGAAATTTGTGGCAAAACAAA 222
XX TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
XX DB 397 GAAACAGTATGTTTATAGCAAGCAGTGTATGAAGACTGAAATTTGTGGCAAAACAAA 456
XX
XX 223 CTTCGCAATGGCAGCTTCCAGTATGATTTGTGCCCAAGCAAGAACTCTCAGCAAGCTAT 282
XX TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
XX DB 457 CTTCGCAATGGCAGCTTCCAGTATGATTTGTGCCCAAGCAAGAACTCTCAGCAAGCTAT 516
XX
XX 283 GAAAAGGAAAAGAACTGTGTGCAAAATCTTTAGCAAGTGTGAGATCAATCAAGTG 342
XX TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
XX DB 517 GAAAAGGAAAAGAACTGTGTGCAAAATCTTTAGCAAGTGTGAGATCAATCAAGTG 576
XX
XX 343 GAATTTGTGAACAATCTTATATCCCAATGTGTATTTACAAATGAGGACATATAACTCG 402
XX TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
XX DB 577 GAATTTGTGAACAATCTTATATCCCAATGTGTATTTACAAATGAGGACATATAACTCG 636
XX
XX 403 TATCTTAAACCTATGTTGACAGAGAGATTTCATTAACCTGTGCGAGCTGGGATTTGGAT 462
XX TATCTTAAACCTATGTTGACAGAGAGATTTCATTAACCTGTGCGAGCTGGGATTTGGAT
XX DB 637 TATCTTAAACCTATGTTGACAGAGAGATTTCATTAACCTGTGCGAGCTGGGATTTGGAT 696
XX
XX 463 CATATCGGTGAGAACATTTCTCATACCTGATGCCAAATCATATGCTGCTGAACCTT 522
XX TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
XX DB 697 CATATGCTGAGAACATTTCTCATACCTGATGCCAAATCATATGCTGCTGAACCTT 756
XX
XX 523 GTGTGCAAGAAATGATCGAGTACCTCTGATGGCATGCTGTGGAAGAACTTATTCAG 582
XX TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
XX DB 757 GTGTGCAAGAAATGATCGAGTACCTCTGATGGCATGCTGTGGAAGAACTTATTCAG 816
XX
XX 583 AGAATGCTGACAGACATTTCTGTGTGAGAGAGCTGGCAGAGAAAGATGGGAGAC 642
XX TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
XX DB 817 AGAATGCTGACAGACATTTCTGTGTGAGAGAGCTGGCAGAGAAAGATGGGAGAC 876
XX
XX 643 TATTTATTCAAAAAC 657
XX TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
XX DB 877 TATTTATTCAAAAAC 891
XX
XX
XX RESULT 13
XX AAK51717
XX ID AAK51717 standard; cDNA; 2366 BP.
XX
XX AAK51717;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 262.
XX
XX Human cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukemia;
XX nervous system disorder; arthritis; inflammation; ss.
XX
XX Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US04098.
XX
XX 03-FEB-2000; 2000US-0496914.
XX 27-APR-2000; 2000US-0560875.
XX 20-JUN-2000; 2000US-0598075.
XX 19-JUL-2000; 2000US-0620325.
XX 01-SEP-2000; 2000US-0654936.
XX 15-SEP-2000; 2000US-0663561.
XX 20-OCT-2000; 2000US-0693325.
XX 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
```


QY	43	TTATATCAATTCCTCCAGAGAGAAAGACGTATATATATGGCAACCCCTAGGAATATA	102		
Db	261	TTCCAGAAATTCCTCCAGAGAGAAAGACGTATATATATGGCAACCCCTAGGAATATA	320		
QY	103	CCAGAGAGAATTCCTACTTAGACAGACATPACCAACAGCTGTGCCAGACTCTGTTAAACCA	162		
Db	321	CCAGAGAGAATTCCTACTTAGACAGACATPACCAACAGCTGTGCCAGACTCTGTTAAACCA	380		
QY	163	GAAGACGATATGTTTACAGACGACCTGCTATGAAAGACTGAGATATGTGTGCCAAACAAA	222		
Db	381	GAAGACGATATGTTTACAGACGACCTGCTATGAAAGACTGAGATATGTGTGCCAAACAAA	440		
QY	223	CTTGCCAAATGGCACTTCCAGTATGTATGTGTGCCAAAGCAACGAAACHTCTGCAAGCTAT	500		
Db	441	CTTGCCAAATGGCACTTCCAGTATGTATGTGTGCCAAAGCAACGAAACHTCTGCAAGCTAT	500		
QY	283	GAAGAGGAAGAAAGAACTGTGTCTCAAAATACCTTTAGAGCAGTGTGACAGTCAAGTCA	342		
Db	501	GAAGAGGAAGAAAGAACTGTGTCTCAAAATACCTTTAGAGCAGTGTGACAGTCAAGTCA	560		
QY	343	GAATTTGTGGAAACATTTATATCCCAAAATGTGTCAATACCAAAATGGGACATPAACTCG	402		
Db	561	GAATTTGTGGAAACATTTATATCCCAAAATGTGTCAATACCAAAATGGGACATPAACTCG	620		
QY	403	TATCTTAAACCTATGTGTGACAGAGATTTTCAATACCTGCTTGCCAGCTGGGATTGGAT	462		
Db	621	TATCTTAAACCTATGTGTGACAGAGATTTTCAATACCTGCTTGCCAGCTGGGATTGGAT	680		
QY	463	CATATGCTGAGAAACATTTCTGCATACCTGAGTGATGCAAAATAGTATGTGCTGCAACTT	522		
Db	681	CATATGCTGAGAAACATTTCTGCATACCTGAGTGATGCAAAATAGTATGTGCTGCAACTT	740		
QY	523	GTGTGCAGAGAAATGTCACCGAGTGCCTCTGATGAGCATGTGTGTGAAGAAAGCTTATGAG	582		
Db	741	GTGTGCAGAGAAATGTCACCGAGTGCCTCTGATGAGCATGTGTGTGAAGAAAGCTTATGAG	800		
QY	583	AGAAATGTCAGAGACAGATTCCTCTGTGAGAGAGGCTGTGAGAAAGAAAGATGGGAGCAG	642		
Db	801	AGAAATGTCAGAGACAGATTCCTCTGTGAGAGAGGCTGTGAGAAAGAAAGATGGGAGCAG	860		
QY	643	TATTTATTCAAAAC 657			
Db	861	TATTTATTCAAAAC 875			
RESULT 15					
AAK52699	AAK52699 standard; cDNA; 3003 BP.				
XX	AAK52699;				
XX	06-NOV-2001 (first entry)				
DE	Human polynucleotide SEQ ID NO 2228.				
XX					
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; hematopoiesis; tissue growth factor; immunomodulator; cancer; leukemia; nervous system disorder; arthritis; inflammation; ss.				
XX	Homo sapiens.				
OS	MO200157190-A2.				
PN	09-AUG-2001.				
PD					
PF	05-FEB-2001; 2001MO-US04098.				
XX					
PR	03-FEB-2000; 2000US-0496914.				
PR	27-APR-2000; 2000US-0560875.				
PR	20-JUN-2000; 2000US-0598075.				
PR	19-JUL-2000; 2000US-0620325.				
PR	01-SEP-2000; 2000US-0654936.				

Query Match	92.6%	Score 608.6	DB 22	Length 3003
Best Local Similarity	99.3%	Pred. NO. 1.1e-185		
Matches 611	Conservative 0	Mismatches 4	Indels 0	Gaps 0
43	TTTATGAAATTCCTCAGAGAGAGAAAGACTGTATTAATGGCGAACCCCTAGAGAGATATA	102		
11	TTTATGAAATTCCTCAGAGAGAGAAAGACTGTATTAATGGCGAACCCCTAGAGAGATATA	102		
298	TTCCAGAAATTCCTCAGAGAGAGAAAGACTGTATTAATGGCGAACCCCTAGAGAGATATA	357		
103	CCAGAGAGAAATTCCTCAGAGAGAGAAAGACTGTATTAATGGCGAACCCCTAGAGAGATATA	162		
358	CCAGAGAGAAATTCCTCAGAGAGAGAAAGACTGTATTAATGGCGAACCCCTAGAGAGATATA	417		
163	GAAAGAGATTTGTTAGCAAGCACTGTGTGAAGCTAGAAATTTGTTGGCGAAACAA	222		
418	GAAAGAGATTTGTTAGCAAGCACTGTGTGAAGCTAGAAATTTGTTGGCGAAACAA	477		
223	CTTGGCAATGGCACTTCACATGATGATGTGGCCAGCAAGGAAATCTCAGCAACTAT	282		
478	CTTGGCAATGGCACTTCACATGATGATGTGGCCAGCAAGGAAATCTCAGCAACTAT	537		
283	GAAAGAGAAAGAAAGCACTGTGTGAAGCTAGAAATTTGTTGGCGAAACAA	342		
538	GAAAGAGAAAGAAAGCACTGTGTGAAGCTAGAAATTTGTTGGCGAAACAA	597		
343	GAAATTTGTTGGAACATCTTATATCCCAATGTGTCTATTACCAATGGGCAATAACTCG	402		
598	GAAATTTGTTGGAACATCTTATATCCCAATGTGTCTATTACCAATGGGCAATAACTCG	657		
403	TATCTTTAAACCTATGTTGCAAGAGATTTCAATACCTGCTGCCAGCTGGGATTTGAT	462		
658	TATCTTTAAACCTATGTTGCAAGAGATTTCAATACCTGCTGCCAGCTGGGATTTGAT	717		
463	CATATCGCTGAGAAATTTCTGTCAATACCTGATGATCCAAATCATTATGTTGCTGAACT	522		
718	CATATTTGCTGAGAAATTTCTGTCAATACCTGATGATCCAAATCATTATGTTGCTGAACT	777		
523	GTGTGCAAGGAATGGTACCGAGTACCTGTATGGCATGTGTGGAAGAAAGCTTATCGAG	582		

Db	778	GTGTGCAAGGAATGGTACCGAGTGACCTCTGATGGCATCTGTGGAGAGAACTTATCGAG	837
QY	583	AGAAATGGTCAGAGACAGATTCTCTGTGAGAGGCTGTGCAGAAAGAGAGATGGGACAG	642
Db	838	AGAAATGGTCAGAGACAGATTCTCTGTGAGAGGCTGTGCAGAAAGAGAGATGGGACAG	897
QY	643	TATTTATTCAAAAAC	657
Db	898	TATTTATTCAAAAAC	912

Search completed: August 20, 2003, 09:41:47
Job time : 200.915 secs

THIS PAGE BLANK (USPTO)

FEATURES
source

Location/Qualifiers
1. 851
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6154838"
/tissue="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/note="Organ: eye; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.75 kb. Library constructed by Life
Technologies."

BASE COUNT 243 a 196 c 223 g 188 t 1 others
ORIGIN

Query Match 91.0%; Score 597.6; DB 13; Length 851;
Best Local Similarity 99.2%; Pred. No. 1.3e-157;
Matches 611; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY 43 TTTATGAATTCCTCAGAGAGAGAGACTGTATTAATGCGAACCCTTAGAAGATATA 102
|||
DB 207 TTCCAGAAATTCCTCAGAGAGAGAGACTGTATTAATGCGAACCCTTAGAAGATATA 266
103 CCAGAGAAATTCCTCAGAGAGAGAGACTGTATTAATGCGAACCCTTAGAAGATATA 162
267 CCAGAGAAATTCCTCAGAGAGAGAGACTGTATTAATGCGAACCCTTAGAAGATATA 326
163 GAAACAGATATTTAGCAAGCAGCTGTATGAAGACTGAAATTTGTGCGCAAAACAAA 222
327 GAAACAGATATTTAGCAAGCAGCTGTATGAAGACTGAAATTTGTGCGCAAAACAAA 386
OY 223 CTGCGCAATGGCAGCTTCAGATATGTTTGGCCCAAGCAAGAACTTCAGCAAGCTAT 282
|||
DB 387 CTGCGCAATGGCAGCTTCAGATATGTTTGGCCCAAGCAAGAACTTCAGCAAGCTAT 446
283 GAAAGGAAAGAAAGAACTGTGTCAAAATCTTTAGCAGTGGTGCAGATCAGATCAAGTG 342
447 GAAAGGAAAGAAAGAACTGTGTCAAAATCTTTAGCAGTGGTGCAGATCAGATCAAGTG 506
OY 343 GAAATTTGTGAACATCTTATATCCCAATGTGTCAATTAACAACTGGGACATTAACCTG 402
507 GAAATTTGTGAACATCTTATATCCCAATGTGTCAATTAACAACTGGGACATTAACCTG 566
OY 403 TATCTTAAACCTATGTCAGAGAGAGATTTCACTGCTGCGCAAGCTCGGGGATTTGAT 462
|||
DB 567 TATCTTAAACCTATGTCAGAGAGAGATTTCACTGCTGCGCAAGCTCGGGGATTTGAT 626
463 CATATCGCTGAGAACATTTCTGTCACTACCTGGATGCCAAATCACTATGTGCTGGAACCT 522
627 CATATCGCTGAGAACATTTCTGTCACTACCTGGATGCCAAATCACTATGTGCTGGAACCT 686
OY 523 GTGTGCAAGAGAGATGTACCGAGTACCTGTGATGGCATGCTGTGGAAGAACCTTATGAG 582
687 GTGTGCAAGAGAGATGTGTACCGAGTACCTGTGATGGCATGCTGTGGAAGAACCTTATGAG 746
OY 583 AGAATGTGCAAGAGAGATTTCTGTGGAAGAGGCTTGGCAGAACGAAGAGATGGGG-ACA 641
|||
DB 747 AGAATGTGCAAGAGAGATTTCTGTGGAAGAGGCTTGGCAGAACGAAGAGATGGGGNACA 806
OY 642 GTATTATTCAAAAAC 657
|||
DB 807 GTATTATTCAAAAAC 822

RESULT 2
B1822845 828 bp mRNA linear EST 04-OCT-2001
LOCUS 603040168F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5180993 5',
DEFINITION mRNA sequence.
ACCESSION B1822845
VERSION B1822845.1 GI:15934395
KEYWORDS EST.

SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
NIH-MGC <http://mgl.ncl.nih.gov/>
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM11451 row: h column: 18
High quality sequence stop: 756.

FEATURES
source

Location/Qualifiers
1. 828
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5180993"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age 23-27; 1
male lung, age 27; and 1 male testis, age 66. Library is
oligo-dt primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC library."

BASE COUNT 241 a 187 c 215 g 185 t
ORIGIN

Query Match 89.0%; Score 585; DB 12; Length 828;
Best Local Similarity 97.9%; Pred. No. 4.5e-154;
Matches 604; Conservative 0; Mismatches 10; Indels 3; Gaps 1;

OY 43 TTTATGAATTCCTCAGAGAGAGAGACTGTATTAATGCGAACCCTTAGAAGATATA 102
|||
DB 188 TTCCAGAAATTCCTCAGAGAGAGAGACTGTATTAATGCGAACCCTTAGAAGATATA 247
103 CCAGAGAAATTCCTCAGAGAGAGAGACTGTATTAATGCGAACCCTTAGAAGATATA 162
248 CCAGAGAAATTCCTCAGAGAGAGAGACTGTATTAATGCGAACCCTTAGAAGATATA 307
OY 163 GAAACAGATATTTAGCAAGCAGCTGTATGAAGACTGAAATTTGTGCGCAAAACAAA 222
308 GAAACAGATATTTAGCAAGCAGCTGTATGAAGACTGAAATTTGTGCGCAAAACAAA 367
OY 223 CTGCGCAATGGCAGCTTCAGATATGTTTGGCCCAAGCAAGAACTTCAGCAAGCTAT 282
|||
DB 368 CTGCGCAATGGCAGCTTCAGATATGTTTGGCCCAAGCAAGAACTTCAGCAAGCTAT 427
283 GAAAGGAAAGAAAGAACTGTGTCAAAATCTTTAGCAGTGGTGCAGATCAGATCAAGTG 342
428 GAAAGGAAAGAAAGAACTGTGTCAAAATCTTTAGCAGTGGTGCAGATCAGATCAAGTG 487
OY 428 GAAATTTGTGAACATCTTATATCCCAATGTGTCAATTAACAACTGGGACATTAACCTG 402
488 GAAATTTGTGAACATCTTATATCCCAATGTGTCAATTAACAACTGGGACATTAACCTG 547
OY 403 TATCTTAAACCTATGTCAGAGAGAGATTTCACTGCTGCGCAAGCTCGGGGATTTGAT 462
|||
DB 548 TATCTTAAACCTATGTCAGAGAGAGATTTCACTGCTGCGCAAGCTCGGGGATTTGAT 607
463 CATATCGCTGAGAACATTTCTGTCACTACCTGGATGCCAAATCACTATGTGCTGGAACCT 522

```
Db      608 CATATGCTGAGAACATTTCTGTCATACCTGATGCGCAATCTATGCTGCTCAACTT 667
Oy      523 GTGTGCAAGAAATGTTACGAGTACCTCTGTATGCGCATGCTGTGAGAAAGCTTATGAG 582
Db      668 GTGTGCAAGAAATGTTACGAGTACCTCTGTATGCGCATGCTGTGAGAAAGCTTATGAG 727
Oy      583 AGAATGCTCAGACAGATTTCTGTGTGAGAGGCGCTGGCAGAAAGCAAGAGA---TGGGGA 639
Db      728 AGAATGCTCAGACAGATTTCTGTGTGAGAGGCGCTGGCAGAAAGCAAGAGCATGGGAGC 787
Oy      640 CAGTATTTATTCAAAA 656
Db      788 CAGTATTTATTCAAAA 804

RESULT 3
LOCUS   B0948186      1147 bp      mRNA      linear      EST 21-AUG-2002
DEFINITION AGENCOURT_8878641 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6464639
5', mRNA sequence.
ACCESSION B0948186
VERSION   B0948186.1 GI:22363664
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1147)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM13986 row: a column: 24
High quality sequence stop: 501.
Location/Qualifiers
FEATURES
source
1. 1147
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="6464639"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site:1; NotI;
Site:2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
BASE COUNT      324 a      289 c      284 g      250 t
ORIGIN
Query Match      88.8%; Score 583.2; DB 13; Length 1147;
Best Local Similarity 97.7%; Pred. No. 1.8e-153;
Matches 602; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

Oy      43 TTTATGAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 102
Db      150 TTCCAGAAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 209
Oy      103 CCAGAGAGAAATTCCTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 162
Db      210 CCAGAGAGAAATTCCTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 269
Oy      163 GAAACAGTATGTTTGCAAGACACTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 222
Db      270 GAAACAGTATGTTTGCAAGACACTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 329
```

```
Oy      223 CTTGCCAAATGCGACTTCCAGATATGATTTGTCGCCAAGCAAGGAACTCTCAGCAAGCTAT 282
Db      330 CTTGCCAAATGCGACTTCCAGATATGATTTGTCGCCAAGCAAGGAACTCTCAGCAAGCTAT 389
Oy      283 GAAAAGGAAAGAAAGAACTGTGTCTCAAAATCTTTAGACAGTGGTGCAGAGTCAAGTGC 342
Db      390 GAAAAGGAAAGAAAGAACTGTGTCTCAAAATCTTTAGACAGTGGTGCAGAGTCAAGTGC 449
Oy      343 GAATTTGTGAGAACATCTTATATCCAAAGTGTCAATACCAATAGGCGACATTAACATCG 402
Db      450 GAATTTGTGAGAACATCTTATATCCAAAGTGTCAATACCAATAGGCGACATTAACATCG 509
Oy      403 TATCTTAAACCTATGTTGAGAGAGAGAGATTTCAATACCTGCTGCCAGCTGGGAGATTGAT 462
Db      510 TATCTTAAACCTATGTTGAGAGAGAGATTTCAATACCTGCTGCCAGCTGGGAGATTGAT 569
Oy      463 CATATGCTGAGACAACTTGTCTCATACCTGTGATGCCAAATCACTATGCTCTGCAACTT 522
Db      570 CATATGCTGAGACAACTTGTCTCATACCTGTGATGCCAAATCACTATGCTCTGCAACTT 629
Oy      523 GTGTGCAAGAAATGTTACCGAGTACCTGTGATGGCATGCTGT- GGAAGAGCTTATGCA 581
Db      630 GTGTGCAAGAAATGTTACCGAGTACCTGTGATGGCATGCTGTGGAAGAGCTTATGCA 689
Oy      582 GAGAAATGCTCAGACAGATTTCTGTGTGAGAGGCGCTGGCAGAAAGCAAGAGATGGGAGCA 641
Db      690 GAGAAATGCTCAGACAGATTTCTGTGTGAGAGGCGCTGGCAGAAAGCAAGAGATGGGAGC 749
Oy      642 GTATTTATTCAAAAAC 657
Db      750 GTATTTATTCAAAAAC 765
```

```
RESULT 4
LOCUS   BG722472      752 bp      mRNA      linear      EST 08-MAY-2001
DEFINITION 602693716F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4825970 5',
mRNA sequence.
ACCESSION BG722472
VERSION   BG722472.1 GI:14001659
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 752)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Miklos Palovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGR), Shliraki
Toshinuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10739 row: p column: 03
High quality sequence stop: 728.
Location/Qualifiers
FEATURES
source
1. 752
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="4825970"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/notes="Organ: testis; Vector: pBluescriptPR (modified
pBluescript KS+); Site:1: BamHI; Site:2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3',
```

size-selected for average insert size 2.2 kb and normalized to ROP 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 238 a 143 c 194 g 177 t

Query Match 86.2%; Score 566.4; DB 10; Length 752;
Best Local Similarity 98.8%; Pred. No. 7.7e-149;
Matches 581; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 46 ATGATTCCTCAGAGAGAGAAAGACTGTATATATGCGAAGCCCTAGAGATATATACCA 105
DB 161 AAGAAATTCCTCAGAGAGAGAAAGACTGTATATATGCGAAGCCCTAGAGATATATACCA 220
QY 106 GAGAGAAATTCCTCAGAGAGAAAGACTGTATATATGCGAAGCCCTAGAGATATATACCA 165
DB 221 GAGAGAAATTCCTCAGAGAGAAAGACTGTATATATGCGAAGCCCTAGAGATATATACCA 280
QY 166 ACAGTATGTTAGCAG 225
DB 281 ACAGTATGTTAGCAG 340
QY 226 GCCAATGCGACCTCCAGTATGATGATGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 285
DB 341 GCCAATGCGACCTCCAGTATGATGATGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 400
QY 286 AAGAGAAAG 345
DB 401 AAGAGAAAG 460
QY 346 TTGTGAGACATCTTATATCCCAATGATGATGATGATGATGATGATGATGATGATGATG 405
DB 461 TTGTGAGACATCTTATATCCCAATGATGATGATGATGATGATGATGATGATGATGATG 520
QY 406 CTTAAACCTATGTTGAG 464
DB 521 CTTAAACCTATGTTGAG 580
QY 465 TATGCTGAG 524
DB 581 TATGCTGAG 640
QY 525 GTGCAAG 584
DB 641 GTGCAAG 700
QY 585 AATGCTGAG 632
DB 701 AATGCTGAG 748

RESULT 5 743 bp mRNA linear EST 22-MAY-2001
LOCUS BG829037
DEFINITION 60275336F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4906215 5',
mRNA sequence.
ACCESSION BG829037
VERSION BG829037.1 GI:14176624
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 743)
AUTHORS NTH-MGC http://mgc.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.liml.gov
Plate: L10M1808 row: 0 column: 16
High quality sequence stop: 703.

FEATURES
source

Location/Qualifiers

1..743

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4906215"

/tissue="type="thadomyosarcoma"

/lab host="DH10B (phage-resistant)"

/clone.lib="NTH_MGC_17"

/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 233 a 158 c 179 g 173 t

ORIGIN

Query Match 85.1%; Score 559.2; DB 12; Length 743;
Best Local Similarity 96.4%; Pred. No. 8.2e-147;
Matches 615; Conservative 0; Mismatches 18; Indels 5; Gaps 4;

QY 24 GCAAG 83
DB 79 GCAAG 138
QY 84 ACCCCCTAG 143
DB 139 ACCCCCTAG 198
QY 144 CAGAGCTGCTTAAACCAAG 203
DB 199 CAGAGCTGCTTAAACCAAG 258
QY 204 TTGTGAG 263
DB 259 TTGTGAG 318
QY 264 GAAACTGAG 321
DB 319 GAAACTGAG 378
QY 322 TGATCAG 381
DB 379 TGATCAG 438
QY 382 CAACATGAG 441
DB 439 CAACATGAG 498
QY 442 CTGGCAG 501
DB 499 CTGGCAG 558
QY 502 TCACTATGCTGCTGTAAGTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 561
DB 559 TCACTATGCTGCTGTAAGTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 618
QY 562 CTGTGG-AAG 619
DB 619 CTGTGGAG 678
QY 620 CAG 656

Db	679	CAGAACGAGACGATGGGACAGATATTATTCACAAA	716
RESULT 6			
AK032221			
LOCUS	AK032221	2897 bp	mRNA
DEFINITION	Mus musculus adult male oocyte/ovary brain cDNA, RIKEN full-length enriched library, clone:6430504E23 product:beta-transducin repeat containing protein, full insert sequence.		linear HTC 05-DEC-2002
ACCESSION	AK032221.1	GI:26082733	
VERSION	AK032221.1	GI:26082733	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	Carninci, P. and Hayashizaki, Y.		
AUTHORS	1		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsumata, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasliwal, K., Fujiwaka, S., Inoue, K., Togawa, Y., Iwawa, M., Ohara, E., Matabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsui, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aikawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Ikawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R., Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., Kling, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nakaido, I., Pesole, G., Queckenbush, J., Schirml, L. M., Stubbli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bull, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustinich, S., Hill, D., Hotmann, M., Hume, D. A., Kamita, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazarrelli, J., Mombaerts, P., Nordone, P., Ring, B., Rongwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyokawa, K., Wang, K. H., Weitz, C., Wiltberger, C., Wilmberg, L., Wyszewski, B., A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohsaki, S., and Hayashizaki, Y.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409 (6821), 685-690 (2001)		
MEDLINE	21085560		
PUBMED	11217851		
REFERENCE	5		
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		

JOURLN	REFERENCE	AUTHORS
Nature 420, 563-573 (2002)	6 (bases 1 to 2897)	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, H., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akehira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
COMMENT	Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://tentom.gsc.riken.go.jp/. Location/Qualifiers	
FEATURES	source 1..2897 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="RANTOM:DB:6430504E23" /db_xref="taxon:10090" /clone="6430504E23" /sex="male" /tissue_type="olfactory brain" /clone_id="RIKEN full-length enriched mouse cDNA library /dev:stage="adult"	
BASE COUNT	720 a 736 c 771 g 670 t	
ORIGIN	misc_feature 1..2897 /note="beta-transudcin repeat containing protein (MGI:1338871, GBNM_009771, evidence: BLASTN, 100%, match=1502)"	
Query Match	80.0%; Score 535.4; DB 11; Length 2897;	
Best Local Similarity	90.9%; Pred. No. 6.4e-137;	
Matches 559; Conservative	0; Mismatches 56; Indels 0; Gaps 0;	
43	TTTATGATTCCTGAGAGAGAGACGTATATATGGCGAACCCTTAGGAAGTATA	102
219	TTCCAGATTCTCGAGAGAGAGAGACGTATATATGGCGAACCCTTAGGAAGTATA	278
103	CCAGAGAGAAATTCATTGAGACAGACATACAACAGCTGTGCAGACTTGCTTAAACCA	162
279	CCAGAGAGAAATTCATTGAGACAGACTTACAACAGCTGTGCAGACTTGGATTAACCA	338
163	GAACAGATTTTATAGCAAGACAGCTGTGAAGACTGGAATTTGTGTGCCAACAACAA	222
339	GAGACAGATTTTATAGCAAGACAGCTGTGAAGACTGGAATTTGTGTGCCAACAACCA	398
223	CTTCCCAATGCAATTCACATGATATATTTGGCCCAAGCAAGAACTCTCAGCAAGTAT	282
399	CTTCCCAATGCAATTCACATGATATTTGTGCCCAAGCAGCGAATCTCAGCAAGTAT	458
283	GAAGAGAGAAAGAACTGTGTGTCAAATCTTTGAGCAGTGGTCAAGATCAATCACTG	342
459	GAGAGAGAAAGAGAGCTGTGTGTCAAATTTTGGAGCAGTGGTCAAGATCAATCACTG	518

QY 343 GAATTTGTGGAACATCTTATATCCCAATGTCATTACCAACATGGGCACATTAAGCTCG 402
 Db 519 GAATTTGTAGAACACCTTATATCCCAATGTCATTACCAACATGGGCACATTAAGCTCG 578
 QY 403 TATTTTAACCTATGTCGAGAGATTTCTTAACTGCTGCGACGCTGGGATTTGAT 462
 Db 579 TACCTAAACCTATGTCGAGAGATTTCTTAACTGCTGCGACGCTGGGATTTGAT 638
 QY 463 CATATCCGTCGAGAACATTTCTGTCATACCTGATGCCAAATCTATGTCGTCGAAGTT 522
 Db 639 CACATCGCTGAGAACATTTCTGTCATACCTGATGCCAAATCTATGTCGTCGAAGTT 698
 QY 523 GTGTGCAAGCAATGTCATACCTGATGCCAAATCTATGTCGTCGAAGTT 582
 Db 699 GTGTGCAAGCAATGTCATACCTGATGCCAAATCTATGTCGTCGAAGTT 758
 QY 583 AGAATGTCGAGACAGATTTCTGTCGAGAGAGCTGCGACAGAACAGAGATGGGACAG 642
 Db 759 AGAATGTCGAGACAGATTTCTGTCGAGAGAGCTGCGACAGAACAGAGATGGGACAG 818
 QY 643 TATTTATTCACAAAAC 657
 Db 819 TACTTATTCACAAAAC 833
 RESULT 7
 AK052317 4502 bp mRNA linear HTC 05-DEC-2002
 LOCUS Mus musculus 13 days embryo heart cDNA, RIKEN full-length enriched
 DEFINITION library, clone:0330027011 product:beta-transducin repeat containing
 protein, full insert sequence.
 ACCESSION AK052317
 VERSION AK052317.1 GI:26095121
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
 MEDLINE Genome Res. 10 (10), 1617-1630 (2000)
 PUBMED 20493574
 REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M.,
 Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
 Yonekura, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuzawa, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 JOURNAL sequencing pipeline with 384 multiplexed capillary sequencer
 MEDLINE Genome Res. 10 (11), 1757-1771 (2000)
 PUBMED 20530913
 REFERENCE 4
 AUTHORS Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
 Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S.,
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
 Flischnmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
 Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G.,

Quackenbush, J., Schirml, L. M., Staubli, F., Suzuki, R., Tomita, M.,
 Wagner, L., Washio, T., Sakai, R., Okido, T., Furuno, M., Aono, H.,
 Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
 Carninci, P., De Bonaldo, M. F., Brownstein, J. C., Bull, C.,
 Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
 Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
 Marchionni, L., Mashima, J., Mazzarelli, J., Mombaeets, P., Nordone, P.,
 Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
 Sato, K., Schonbach, C., Sessa, T., Shibata, Y., Storch, K. F., Suzuki, H.,
 Toyooka, K., Wang, R. H., Weltz, C., Whitaker, C., Wilmink, L.,
 Wyszewski, B., Yoshida, K., Hasegawa, Y., Kawai, H., Kohzuki, S.,
 and Hayashizaki, Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 TITLE Group Phase I & II Team.
 ANALYSIS Analysis of the mouse transcriptome based on functional annotation
 JOURNAL of 60,770 full-length cDNAs
 MEDLINE Nature 420, 563-573 (2002)
 PUBMED 12466851
 REFERENCE 6
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Aizawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hirose, T., Hirose, T.,
 Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kondo, M.,
 Koyu, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnishi, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Tanahashi, F., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M., and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-rsgsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/
 FEATURES
 SOURCE Location/Qualifiers
 1. 4502
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM:DB:330027D11"
 /db_xref="taxon:10090"
 /clone_id="D330027D11"
 /tissue_type="heart"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="13 days embryo"
 1. 4502
 /note="beta-transducin repeat containing protein
 (MD|GRI:1338871, GRI|NM_009771, evidence: BLASTN, 100%,
 match=1502)"
 misc_feature
 BASE COUNT 1284 a 998 c 1126 g 1094 t .
 ORIGIN
 Query Match 80.0%; Score 525.4; DB 11; Length 4502;
 Best Local Similarity 90.9%; Pred. No. 8.3e-117;
 Matches 559; Conservative 0; Mismatches 56; Gaps 0;

Oy	43	TTTATGATTCCTCAGAGAGAAAGACGTAAATATGGCGAAACCCCTAGGAAAGTATA	102
Db	280	TTCCAGATTTCTCAGAGAGAAAGACGTAAATATGGCGAAACCCCTAGGAAAGTATA	339
Oy	103	CCAGAGAAAGATTCACCTAGACAGACATACAAACAGCTGTGGCAGACTGTGTTAAACCA	162
Db	340	CCAGAGAAAGATTCACCTAGACAGACACTTACAAACAGCTGTGGCAGACTTGTGATMAACCA	399
Oy	163	GAAACAGATGTTTAGCAGACAGCTGCTATGGAAGACTGGAATTTGTGGCCAAAACAAA	222
Db	400	GAGACAGATGTTTAGCAGACAGCTGCTATGGAAGACTGGAATTTGTGTGGCCAAAACAAA	459
Oy	223	CTTGCAGATGGCAGCTCCAGTATGTTGTGGCCAAAGCAAGCAAGCAAGTAT	282
Db	460	CTTGCAGATGGCAGCTCCAGCAGTATGTTGTGGCCAAAGCAAGCAAGTAT	519
Oy	283	GAAAAAGAAAAGAACTGTGTCAAAATCTTTGAGCAGTGGTCCAGATCAGATCAAGTG	342
Db	520	GAGAAAGAAAAGAGCTGTGTCAAAATCTTTGAGCAGTGGTCCAGATCAGATCAAGTG	579
Oy	343	GAAATTTGTGGAACATCTTATATCCCAATGTGTCTATTACCAACATGGCCACATAACTCG	402
Db	580	GAAATTTGTGGAACACCTTATATCCCAATGTGTCTACTCCAGACATGGCCACATCAACTCC	639
Oy	403	TATCTTAAACCTATGTTGCAGAGAGATTTCACTAACTGGTCCAGCTCGGGGATTTGAT	462
Db	640	TACCTAAACCTATGTTGCAGAGAGATTTCACTAACTGGTCCAGCTCGGGGATTTGAT	699
Oy	463	CATATCGCTGAGAACATTTCTGTCAATACCTGGATGGCAATCATATGTGCTGTAACCTT	522
Db	700	CACATCGCTGAGAACATTTCTGTCAATACCTGGATGGCAATCATATGTGCTGTAACCTT	759
Oy	523	GTTGGCAAGAAATGTTACCGAGTACCTCTATGGCATGCTGTGGAAAGACTTATCGAG	582
Db	760	GTTGGCAAGAAATGTTACCGGCTAGCGTACCGGCAAGCTGTGGAAAGACTTATCGAG	819
Oy	583	AGAAATGGTCAGACAGATTTCTGTGTGAGAGAGCCCTGGCAGAGAAAGATGGGAGAC	642
Db	820	AGAAATGGTCAGACAGCACTCTGTGTGGAGAGCCCTGGCAGAGAGCAAGGCTGGGAGAC	879
Oy	643	TATTTATTTCAAAAAC	657
Db	880	TACTTATTTCAAAAAC	894
RESULT 8			
LOCUS	AK083257	2970 bp	mRNA
DEFINITION			linear HTC 05-DEC-2002
VERSION			
KEYWORDS			Mus musculus adult male hippocampus cDNA, RIKEN full-length
SOURCE			enriched library, clone:C63011X01 product:beta-transducin repeat
ORGANISM			containing protein, full insert sequence.
REFERENCE			AK083257
AUTHORS			AK083257.1 GI:26101148
TITLE			HTC: CAP trapper.
JOURNAL			Mus musculus (house mouse)
MEDLINE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
PUBMED			Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE			1
AUTHORS			Carninci,P. and Hayashizaki,Y.
TITLE			High-efficiency full-length cDNA cloning
JOURNAL			Meth. Enzymol. 303, 19-44 (1999)
MEDLINE			99279253
PUBMED			10349636
REFERENCE			2
AUTHORS			Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
TITLE			Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
JOURNAL			Normalization and subtraction of cap-trapper-selected cDNAs to
MEDLINE			prepare full-length cDNA libraries for rapid discovery of new genes
PUBMED			Genome Res. 10 (10), 1617-1630 (2000)
REFERENCE			1
AUTHORS			Genome Res. 10 (10), 1617-1630 (2000)
TITLE			Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL			Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE			20499374
PUBMED			11042159

REFERENCE AUTHORS	TITLE	JOURNAL MEDLINE PUBMED REFERENCE AUTHORS
3 Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Teshiro, H., Itoh, M., Suni, N., Ishii, T., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunaga, H., Sakaiguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, K., Ozawa, M., Ohara, E., Matsubuchi, M., Yoneeda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Genome Res. 10 (11), 1757-1771 (2000)	
4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamada, T., Salto, T., Katsuda, Y., Gojodori, T., Bono, H., Kasukawa, T., Salto, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiya, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Stabili, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldairelli, R., Barish, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gastlrich, S., Hill, D., Hotmann, M., Hume, D.A., Kamuya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Momberts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-Oka, K., Wang, K.H., Weitz, C., Whiteaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohlsukl, S. and Hayashizaki, Y.	Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)	
5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)	
JOURNAL REFERENCE AUTHORS	6 (bases 1 to 2970) Adachi, J., Aizawa, K., Akiyama, T., Arakawa, T., Bono, H., Carninci, P., Katsuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, I., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kachi, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, K., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Salto, R., Salto, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyo, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	
TITLE JOURNAL	Direct Submission Submitted (16-Apr-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/ , Tel: 81-45-503-9222, Fax: 81-45-503-9216)	
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ Location/Qualifiers	
FEATURES		


```

OY 481 CTGTCAATACGTGATGCCAAATCACTATATGCTGTGACATTTGTGTGCAAGAAATGTAC 540
DB 528 CTGTCAATACGTGATGCCAAATCACTATATGCTGTGACATTTGTGTGCAAGAAATGTAC 587
OY 541 CGAGTACCTGTGATGCTGTGTGCAAGAAATGTATTCAGAGAA 586
DB 588 CGCGTACGTGAGAGCGCATGTGTGTGACAAAGCATATCAGAGAGA 633

RESULT 10
BGS18761 789 bp mRNA linear EST 02-APR-2001
LOCUS 602578346F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491843 5'
DEFINITION mRNA sequence.
ACCESSION BGS18761
VERSION BGS18761.1 GI:13513945
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@bbsr@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM8536 row: k column: 12
High quality sequence stop: 587.
Location/Qualifiers
1. 789
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CECH 11"
/db_xref="taxon:10090"
/clone="IMAGE:3491843"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/clone_11b="NCI_CGAP_Lu29"
/note="Organ: Lung; Vector: PCMV-SF0RT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 257 a 176 c 202 g 154 t

ORIGIN
Query Match 75.6%; Score 496.4; DB 10; Length 789;
Best Local Similarity 89.3%; Pred. No. 4.7e-129;
Matches 591; Conservative 0; Mismatches 66; Indels 5; Gaps 5;

```

```

DB 186 AGCACTGCTATGAGACTGAAAAATTTGTGTGCCCCAAAGCCAACTTGCCAAATGGCACTCC 245
OY 241 AGTATGATTTGTCGCCAAGCAAGAACTCTCAGCAAGTATGAAAGAA -AAGAACT 299
DB 246 AGCATGATTTGTGCCAAGCAGCGGAAACTCTAGCAAGTATGAAAGAAAGAGAGACT 305
OY 300 GTGTGCAAAATCTTTGAGCAGTGTGTGAGAGTCAAGTGG -AATTTGTGAAATC 358
DB 306 GTGTGCAAGTATTTGAGCAGTGTGTGAGAGTCAAGTGGAAATTTGTGAAACACC 365
OY 359 TTATATCCCAATGTCTATTTACCAACATGGCCACATTAACCTGATCTTAACCTATGT 418
DB 366 TTATATCCCAATGTCTATTTACCAACATGGCCACATTAACCTGATCTTAACCTATGT 425
OY 419 TGCAGAGATTTCAATTAACCTGCTGCCAGCTCGGGGATTTGGATCATATATCGCTGAGACA 478
DB 426 TGCAGAGATTTCAATTAACCTGCTGCCAGCTCGGGGATTTGGATCATATATCGCTGAGACA 485
OY 479 TTCTGTCAATACCTGATGCAATATCACTATATGCTGTGAACTGTGTGCAAGAAATGT 538
DB 486 TTCTGTCAATACCTGATGCAATATCACTATATGCTGTGTGAGCTCGTGTGCAAGAAATGT 545
OY 539 ACCG-AGTACCTGTGTGAGCATGCTGTGAAAGAACTTATGAGAGAAATGTCTAGAGC- 596
DB 546 ACCGAGTGTACGTGCGAGCGCATGTGTGTGAAAAAAGCTATGAGAGAGTGTCTAGAGC 605
OY 597 ACATTTCTGTGTGA-GAGGCTGTGCGAGAAAGAGAGATGGGAGCATTTATTCAAA 655
DB 606 GCCTACTGTGTGAGCAGGCGCCGCGAGAGCGAGAGCTGGGACAGACTTACTCAAAAC 665
OY 656 AC 657
DB 666 AC 667

```

```

RESULT 11
BF076123 521 bp mRNA linear EST 25-APR-2001
LOCUS 225612 MARC 280V Bos taurus cDNA 5', mRNA sequence.
DEFINITION BF076123
ACCESSION BF076123.1 GI:10869667
VERSION BF076123.1 GI:10869667
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 521)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A., Chitko-McKoy,C.G.,
Peters,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keefe,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
JOURNAL MEDLINE 21180013
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross-match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACAT
BACKWARD: GTTTCCAGTCAGACG
Plate: 85 row: E column: 23
Seq primer: ATTTAGTGACACTATAG.
Location/Qualifiers

```

	source	1..521	/organism="Bos taurus"
			/mol_type="mRNA"
			/db_xref="taxon:9913"
			/tissue_type="pooled"
			/lab_host="DH10B"
			/clone_id="MARC_2BOV"
			/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
			library made from pooled tissue from testis, thymus,
			semitendinosus muscle, longissimus muscle, pancreas,
			adrenal, and endometrium."
BASE COUNT	170 a	105 c	116 g
ORIGIN			130 t
Query Match	73.6%	Score 483.8;	DB 10; Length 521;
Best Local Similarity	95.8%;	Pred. No. 1.4e-125;	
Matches 497:	Conservative 0;	Mismatches 22;	Indels 0; Gaps 0;
OY	49	AATTCCTGAGAGAGAGAAGCATTAATAATGGCGAACCCCTAGCAACATAATACCAGAG	108
Db	3	AATTCCTGAGAAAGGAAGACTGTATATATGGCGAACCCTTAGGAATATATACCAAG	62
OY	109	AAGAATTCACTTACAGACATATACAACAGCTGTGCCACACTCTGCTTAACACAGAAACA	168
Db	63	AAGATTCACTTACAGACATATACAACAGCTGTGCCACACTCTGCTTAATCAAGAGACA	122
OY	169	GTA TGTTAGCAAGCAGCTGTATGANAAGCTGAGAA TTGTGGCCAAAACAAACTTGCC	228
Db	123	GTA TGCTAGCAAGCAGCTGTATGANAAGCTGAGAA TTGTGGCCAAAACAAACTTGCC	182
OY	229	AATGCACATTCACAGTATGATTTGTGCCCAAGCAAGGAACCTCACGAAGCTATGAAAG	288
Db	183	AATGCACATTCACAGTATGATTTGTGCCCAAGCAAGGAACCTCACGAAGCTATGAAAG	242
OY	289	GAAAAAGAACTGTGTGTCMAATACTTTGAGCAGTGTGAGATCAGATCAAGTGGAAATT	348
Db	243	GAAAAAGAACTGTGTGTCMAATACTTTGAGCAGTGTGAGATCAGATCAAGTGGAAATT	302
OY	349	GTGGAACATCTTATATCCCAGAAATGTGTCAATTACCAACATGGGCAATAAACTCGATCTT	408
Db	303	GTGGAACATCTTATATCCCAGAAATGTGTCAATTACCAACATGGGCAATAAACTCATCTT	362
OY	409	AAACCTAATGTGCAGAGAGATTTTCAATCTGCTCTGCCAGCTCGGGGATTTGGATCATATC	468
Db	363	AAACCTAATGTGCAGAGAGATTTTCAATCTGCTCTGCCAGCTCGGGGATTTGGATCATATC	422
OY	469	GCTGAGAACATCTGTCTCATCTTACCTGGATCCCAAATCATCATGTCGTGAACCTGTGTC	528
Db	423	GCTGAGAACATCTGTCTCATCTTACCTGGATCCCAAATCATCATGTCGTGAACCTGTGTC	482
OY	529	AAGGAATGTACCGAGTAGCTCTGTANTGGATGCTGTGG	567
Db	483	AAAGAAATGTACCGAGTAGCTCTGTANTGGATGCTGTATGG	521
RESULT 12			
LOCUS	Bf781002	658 bp	mRNA linear EST 12-JAN-2001
DEFINITION	60210663JF1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:425310		
ACCESSION	Bf781002		
VERSION	Bf781002.1	GI:12086035	
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	NIH-MGC http://ngc.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabsr@emil.nih.gov		

LOCUS	AL707470	556 bp	mRNA	linear	EST 12-JUN-2003
Query Match	Best Local Similarity	71.8%;	Score 471.4;	DB 10;	Length 658;
Matches 524;	Conservative	0;	Mismatches 51;	Indels 2;	Gaps 2;
43	TTTATGAAATTCCTCAGAGAGAGAAACACGTATATATGGCGAAGCCCTTAGGAAGTATA	102			
84	TTCCGAATTCCTCAGAGAGAGAAACACGTATATATGGCGAAGCCCTTAGGAAGTATA	143			
103	CCAGAGAAATTCACCTTAGACAGACATACAACACAGCTGTGCAGACCTGTGCTTAACCAA	162			
144	CCAGAGAAATTCACCTTAGACAGACATACAACACAGCTGTGCAGACCTGTGCTTAACCAA	202			
163	GAAACAGATGTTTACGCAAGCAGCTGCTATGAAGACTGAGAAATGTGTGGCCAAACAAA	222			
203	GAGACAGATGCTTCAACAGCAGCTGCTATGAAGACTGAAATTTGTGGCCAAACCAA	262			
223	CTTGGCAATGGACATCCAGTATGATGATGAGGCCAAGCAAGGAAACTGACAGACGTAT	282			
263	CTTGGCAATGGACATCCAGTATGATGATGAGGCCAAGCAAGGAAACTGACAGACGTAT	322			
283	GAAAAAGAAAGAACTGTGTGCAAAATACATTGAGCAGTGTGTCAGATCAGATCAAGTG	342			
323	GAGAGAGAAAGAACTGTGTGCAAAATACATTGAGCAGTGTGTCAGATCAGATCAAGTG	382			
343	GAAATTTGGGGAACATCTTATATCCCAATATGCTCTTATACCAATATGGGACATTAACCTG	402			
383	GAA-TTGTAGAACACCTTATATCCCAATATGCTCTTATACCAATATGGGACATTAACCTG	441			
403	TATCTTAAACCTATGTCAGAGAGATTTCAATACCTGCTGCCAGCTCGGGATTTGGAT	462			
442	TACCTAAACCTATGTCAGAGAGATTTCAATACCTGCTGCCAGCTCGGGATTTGGAT	501			
463	CATATCGGTGAGAACATTTGTGATATACCTGGATGGCAATATCACTATGTGCTGTAATTT	522			
502	CACATCGGTGAGAACATTTGTGATATACCTGGATGGCAATATCACTATGTGCTGTAATTT	561			
523	GTGTGCAAGCAATGTTACCGAGTGCACCTGTGATGGCATGCTGTGGAAGAACTTATGAG	582			
562	GTGTGCAAGCAATGTTACCGAGTGCACCTGTGATGGCATGCTGTGGAAGAACTTATGAG	621			
583	AGATGTCAGAGACAGATTTCTGTGTGAGAGAGCCCTGG	619			
622	AGGATGTCAGAGACAGATTTCTGTGTGAGAGAGCCCTGG	658			


```

Oy 163 GAACAGTATGTTAGCAAGCAGCTGATGAGACTGAGAAATGTGTGGCCAAACAAA 222
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 GAGACAGTATGTTAGCAAGCAGCTGATGAGACTGAGAAATGTGTGGCCAAACAAA 417
Oy 223 CTTCAGTATGTTAGCAAGCAGCTGATGAGACTGAGAAATGTGTGGCCAAACAAA 282
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 418 CTTCAGTATGTTAGCAAGCAGCTGATGAGACTGAGAAATGTGTGGCCAAACAAA 477
Oy 283 GAAAAAGAAAAAGAACTGTGTGTCAAAATCTTGTGAGAGTGTGAGAGTCAAGTGTG 342
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 478 GAGAAAGAAAAAGAACTGTGTGTCAAAATCTTGTGAGAGTGTGAGAGTCAAGTGTG 537
Oy 343 GAATTTGTGAGAACTGTTATATCCCAATGTGTGATACCAACATGGGCAATTAATCG 402
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 538 GAATTTGTGAGAACTGTTATATCCCAATGTGTGATACCAACATGGGCAATTAATCG 597
Oy 403 TATCTTAACCTATGTTAGCAAGCAGCTGATGAGACTGAGAAATGTGTGGCCAAACAAA 462
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 598 TACCTAAACCTATGTTAGCAAGCAGCTGATGAGACTGAGAAATGTGTGGCCAAACAAA 657
Oy 463 CATATGCTGAGAACTGTTATATCCCAATGTGTGATACCAACATGGGCAATTAATCG 522
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 658 CACATGCTGAGAACTGTTATATCCCAATGTGTGATACCAACATGGGCAATTAATCG 717
Oy 523 GTGTGCAAGAAATGTGTGATACCAACATGGGCAATTAATCG 578
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 718 GTGTGCAAGAAATGTGTGATACCAACATGGGCAATTAATCG 773

RESULT 15
CD350839 779 bp mRNA linear EST 29-MAY-2003
DEFINITION UT-M-G10-c99-f-10-0-UT.1 NIH_BMAP_G10 Mus musculus cDNA clone
IMAGE: 6852971 5', mRNA sequence.
ACCESSION CD350839
VERSION CD350839.1 GI:31142258
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 779)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: c99pds-femail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.owa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: PYX-5.
Location/Qualifiers
1. 779
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6852971"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_id="NIH_BMAP_G10"
/note="Organ: Brain; Vector: PYX-Asc; Site: 1; Ecor I;
Site_2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was

```

```

size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into PYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGCAG. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System", supported by National
Institute of Mental Health (NIMH), Hemlin Chlin, Ph.D.,
program coordinator."
BASE COUNT 209 a 190 c 201 g 174 t 5 others
ORIGIN
Query Match 68.2% Score 448.2; DB 14; Length 779;
Best Local Similarity 89.9% Pred. No. 2e-115;
Matches 480; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

124 CAGCATACCAACACTGTGCGAGCTGCTGTTAACCAGAAAGATGTTGCAAGC 183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
110 CAGACTTACCAACACTGTGCGAGCTGCTGTTAACCAGAAAGATGTTGCAAGC 169
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 184 ACTGCTATGAAAGACTGGAATTTGTGTGGCCAAACAACTTGGCAATGGCACTTCAGT 243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 170 ACTGCTATGAAAGACTGGAATTTGTGTGGCCAAACAACTTGGCAATGGCACTTCAGC 229
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 244 ATGATTTGCCCAAGCAAGCAAACTCTCAGCAAGCTATGAAAGAAAGAACTGTGT 303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 230 ATGATTTGCCCAAGCAAGCAAACTCTCAGCAAGCTATGAAAGAAAGAACTGTGT 289
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 304 GTCAATACTTTGAGAGTGTGAGTGTGAGTCAAGATCAAGTGAATTTGTGAACATCTATA 363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 290 GTCAAGTATTTTGGAGCTGTGAGTGTGAGTCAAGTGAATTTGTGAACATCTATA 349
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 364 TCCCAAAATGTGTCTATTAACAACATGGGCAATTAACCTGATCTTAACCTATGTCAG 423
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 350 TCCCAAAATGTGTCTATTAACAACATGGGCAATTAACCTGATCTTAACCTATGTCAG 409
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 424 AGAATTTCAATTAATGCTGTGCGCAAGCTGCGGAGTGTGATATATACCTGTGAGAACTGTG 483
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 410 AGGATTTCAATTAATGCTGTGCGCAAGCTGCGGAGTGTGATATATACCTGTGAGAACTGTG 469
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 484 TCATACCTGATGCCAATATCATATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 470 TCATACCTGATGCCAATATCATATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 529
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 544 GTGACCTCTGATGGCAGTGTGTGAGAACTTATCGAGAAATGGTCAAGAGATTCCT 603
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 530 GTGACCTCTGATGGCAGTGTGTGAGAACTTATCGAGAAATGGTCAAGAGATTCCT 589
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 604 CTGTGAGAGAGCCCTGCGAGAAAGAGATGGGAGACATTTATTTCAAAAAC 657
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 590 CTGTGAGAGAGCCCTGCGAGAGCGAGAGGCTGGGAGACATTTATTTCAAAAAC 643
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Search completed: August 20, 2003, 09:29:57
 Job time : 1601.04 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 05:23:39 ; Search time 44.6996 Seconds

(without alignments)
6487.499 Million cell updates/sec

Title: US-10-023-530-1

Perfect score: 657
Sequence: 1 atggaccgcggccggagcgcgt.....gacagatattatcaaaac 657

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued_Patents_NA.*
1: /cgn2_6/ptodata/2/1na/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/1na/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/1na/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/1na/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/1na/PCrus.COMB.seq:*
6: /cgn2_6/ptodata/2/1na/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124.4	18.9	126	3	US-09-172-841-2
2	124.4	18.9	126	4	US-08-951-621-2
3	43.8	6.7	7216	1	US-08-232-463-14
4	35.4	5.4	10881	4	US-09-357-206A-9
5	35.4	5.4	12286	4	US-09-357-206A-1
6	34.6	5.3	1848	1	US-08-313-553-10
7	34.6	5.3	1848	3	US-08-767-993-10
8	34.6	5.3	2246	3	US-09-032-742-3
9	34.6	5.3	2246	3	US-09-032-742-21
10	34.6	5.3	2246	3	US-09-032-742-22
11	34.6	5.3	2246	3	US-09-032-742-24
12	34.6	5.3	2246	3	US-09-032-742-25
13	32	4.9	660	4	US-09-134-001C-2805
14	31.6	4.8	4281	4	US-09-357-206A-8
15	30.6	4.7	799	4	US-09-149-476-288
16	30.6	4.7	1002	4	US-09-328-352-3574
17	30.2	4.6	7400	1	US-08-261-663A-1
18	30.2	4.6	7400	5	PCT-US95-07754A-1
19	30	4.6	3540	4	US-09-107-532A-2472
20	29.6	4.5	124884	4	US-09-661-596A-76
21	29.6	4.5	1230025	4	US-09-158-452A-1
22	29.4	4.5	759	4	US-09-328-352-3199
23	29.2	4.4	4693	3	US-09-359-756-1
24	29.2	4.4	7451	3	US-08-684-672-23
25	29.2	4.4	15016	4	US-09-601-198-60
26	29	4.4	552	4	US-09-252-991A-9856
27	29	4.4	821	3	US-08-235-836C-135

28	29	4.4	839	3	US-08-642-807A-30	Sequence 30, Appl
29	29	4.4	3253	4	US-09-759-359A-1	Sequence 1, Appl
30	29	4.4	319608	4	US-09-539-333D-1	Sequence 1, Appl
31	29	4.4	319608	4	US-09-679-409-1	Sequence 1, Appl
32	28.8	4.4	2784	3	US-08-845-256-9	Sequence 9, Appl
33	28.8	4.4	2784	3	US-08-990-571-9	Sequence 9, Appl
34	28.8	4.4	2784	3	US-08-723-142A-9	Sequence 9, Appl
35	28.8	4.4	2784	4	US-09-526-784A-9	Sequence 9, Appl
36	28.8	4.4	2784	4	US-09-569-098A-9	Sequence 9, Appl
37	28.6	4.4	5385	4	US-09-221-017B-972	Sequence 972, App
38	28.4	4.3	1179	3	US-09-247-373B-43	Sequence 43, Appl
39	28.4	4.3	2169	4	US-09-434-408-3	Sequence 27, Appl
40	28.4	4.3	9100	3	US-08-743-637B-27	Sequence 27, Appl
41	28.4	4.3	9100	3	US-08-526-840B-27	Sequence 27, Appl
42	28.4	4.3	1230025	4	US-09-198-452A-1	Sequence 1, Appl
43	28.4	4.3	1830121	4	US-09-557-884-1	Sequence 1, Appl
44	28.4	4.3	1830121	4	US-09-643-980A-1	Sequence 1, Appl
45	28.2	4.3	828	4	US-09-232-160-7	Sequence 7, Appl

ALIGNMENTS

```
RESULT 1
US-09-172-841-2
; Sequence 2, Application US/09172841
; Patent No. 6232081
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeffrey W.
; APPLICANT: Elledge, Stephen J.
; TITLE OF INVENTION: F-BOX PROTEINS AND GENES
; FILE REFERENCE: BCM-03510
; CURRENT APPLICATION NUMBER: US/09/172,841
; EARLIER FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,621
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 126
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-172-841-2

Query Match      18.9% Score 124.4; DB 3; Length 126;
Best Local Similarity 99.2%; Pred. No. 2.7e+33;
Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      442 CTGCCAGCTCGGGGATGATCATATCGCTGAGAACATTCGTCTACCTGATGCCAA 501
      |||
DB      1 CTGCCAGCTCGGGGATGATCATATTCGTCTGAGAACATTCGTCTACCTGATGCCAA 60

QY      502 TCACATATGTCGCTGCAACTTGTGTGCAAGAAATGTACCGAGTACCTGTGATGGCATG 561
      |||
DB      61 TCACATATGTCGCTGCAACTTGTGTGCAAGAAATGTACCGAGTACCTGTGATGGCATG 120

QY      562 CTGTGG 567
      |||
DB      121 CTGTGG 126

RESULT 2
US-08-951-621-2
; Sequence 2, Application US/08951621
; Patent No. 6573094
; GENERAL INFORMATION:
; APPLICANT: HARPER, JEFFREY W.
; APPLICANT: ELLEDGE, STEPHEN J.
; TITLE OF INVENTION: F-BOX GENES AND PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
```

```

: CITY: San Francisco
: STATE: California
: COUNTRY: United States of America
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/951,621
: FILING DATE: 16-OCT-1997
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: MacKnight, Kamrin T.
: REGISTRATION NUMBER: 38,230
: REFERENCE/DOCKET NUMBER: BCM-02999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 705-8410
: TELEFAX: (415) 397-8338
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 126 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: other nucleic acid
: DESCRIPTION: /desc = "DNA"
: US-08-951-621-2

Query Match      18.98; Score 124.4; DB 4; Length 126;
Best Local Similarity 99.28; Pred. No. 2,7e-33;
Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 442 CTCGACGCTGGGATGATCATATGCTGAGAACATCTGTCATCTGATGCCAA 501
DB 1 CTCGACGCTGGGATGATCATATGCTGAGAACATCTGTCATCTGATGCCAA 60
OY 502 TCACATATGCTGCTGTAACCTGCTGTCAGAGAAATGTAACGAGTACCTCTGATGCGATG 561
DB 61 TCACATATGCTGCTGTAACCTGCTGTCAGAGAAATGTAACGAGTACCTCTGATGCGATG 120
OY 562 CTGTGG 567
DB 121 CTGTGG 126

RESULT 3
US-08-232-463-14/C
: Sequence 14, Application US/08232463
: Patent No. 5670367
: GENERAL INFORMATION:
: APPLICANT: DORNER, F.
: APPLICANT: SCHEIFLINGER, F.
: APPLICANT: FALKNER, F. G.
: TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardner
: STREET: 1800 Diagonal Road, Suite 500
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22313-0299
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/232,463
: FILING DATE:
: CLASSIFICATION: 435
```

```

: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/935,313
: FILING DATE:
: APPLICATION NUMBER: EP 91 114 300.6
: FILING DATE: 26-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: BENT, Stephen A.
: REGISTRATION NUMBER: 29,768
: REFERENCE/DOCKET NUMBER: 30472/114 IMMU
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-9300
: TELEFAX: (703) 683-4109
: TELEX: 899149
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7218 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: CLONE: PT29PL-F15
: US-08-232-463-14

Query Match      6.78; Score 43.8; DB 1; Length 7218;
Best Local Similarity 1.78; Pred. No. 0.00022;
Matches 6; Conservative 207; Mismatches 144; Indels 0; Gaps 0;

OY 13 GAGCGGTGCTGCGAGAGACGACATCAATTTATGAAATCCACAGAGAGAACTGT 72
DB 1416 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1357
OY 73 AATAATGCGAACCCTAGGAAGATATACAGAGAAATTCATAGACAGACATAC 132
DB 1356 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1297
OY 133 AACAGCTGCTCCGACCTCTCTTAACCAAGAACTATGTTAGCAACACTGCTATG 192
DB 1296 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1237
OY 193 AAGACTGAAATGTGTGCGCAAAACAACTTGCCAACTGCACTTCATGATGTTG 252
DB 1236 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1177
OY 253 CCAAGCAGCAAACTCTCAGCAGCTATGAAAGAAAGAACTGCTCAATAC 312
DB 1176 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1117
OY 313 TTGAGCAGTGTGAGCTCAGATCAATGGAATTTGTGAACATCTTATATCCAA 369
DB 1116 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1060

RESULT 4
US-09-357-206A-9/C
: Sequence 9, Application US/09357206A
: Patent No. 6372962
: GENERAL INFORMATION:
: APPLICANT: Dinesh-Kumar, S.
: APPLICANT: Baker, Barbara
: TITLE OF INVENTION: Pathogen Resistance in Plants using cDNA-N/Inton Constructs
: FILE REFERENCE: 042250/191805 (5830-5)
: CURRENT FILING DATE: 1999-07-20
: PRIOR FILING DATE: US 60/093,494
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: Patentin version 3.0
: SEQ ID NO 9
: LENGTH: 10881
: TYPE: DNA
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: Artificial construct of PN / c-DNA-N / Inton 3 / 3'-GRS
```



```

1 NAME/KEY: mutation
2 LOCATION: replace(213, "")
3 OTHER INFORMATION: /note="G to A mutation removes
4 OTHER INFORMATION: AlwNI restriction site."
5 FEATURE:
6 NAME/KEY: misc_feature
7 LOCATION: 1732..1734
8 OTHER INFORMATION: /note="Codon encoding the
9 OTHER INFORMATION: C-terminal amino acid of the rat serotonin
10 OTHER INFORMATION: receptor protein (Type 1c)."
```

```

11 NAME/KEY: misc_signal
12 LOCATION: 374
13 OTHER INFORMATION: /note="RNA start site."
```

```

14 FEATURE:
15 NAME/KEY: CDS
16 LOCATION: 376..1734
17 FEATURE:
18 NAME/KEY: terminator
19 LOCATION: 1735..1737
20 OTHER INFORMATION: /note="Serotonin stop codon."
```

```

21 FEATURE:
22 NAME/KEY: repeat_region
23 LOCATION: 436..462
24 OTHER INFORMATION: /note="Sequence encoding
25 Patent No. 5641650
26 OTHER INFORMATION: polyaspartic acid."
```

```

27 FEATURE:
28 NAME/KEY: mutation
29 LOCATION: replace(1755, "")
30 OTHER INFORMATION: /note="C to T mutation removes
31 OTHER INFORMATION: AlwNI restriction site."
```

```

32 US-08-313-553-10
33
34 Query Match 5.3%; Score 34.6; DB 1; Length 1848;
35 Best Local Similarity 52.4%; Pred. No. 0.15;
36 Matches 76; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
```

```

37 QY 11 CCGAGCGGCTCTCCAGAGAGGCACTCAAGTTATGATTCCTCAGAGAGAGACT 70
38 111111 111111 111111 111111 111111 111111 111111 111111
39 Db 1115 CCGAGGAGGAAGTGGCTAATATGAGCCCTGGAAGCTTCTGMACTGCTGCAAGAAAGT 1174
40 11 111111 111111 111111 111111 111111 111111 111111 111111
41 QY 71 GTATATATGGCGAAGCCCTGGAAGATATATACAGAGAAATTCCTAGACAGACAT 130
42 11 111111 111111 111111 111111 111111 111111 111111 111111
43 Db 1175 GTGGTGAGGAAGAGAAAGAGCTCCGAACCTTAATCCAGATCAGAAACACGCTGAAAGAGA 1234
44 11 111111 111111 111111 111111 111111 111111 111111 111111
45 QY 131 ACAACAGCTGTGCCAGACTGTGCTT 155
46 11 111111 111111 111111 111111 111111 111111 111111 111111
47 Db 1235 AAGAAAGCGTCCAGAGGACACCAT 1259
48 11 111111 111111 111111 111111 111111 111111 111111 111111
```

```

49 RESULT 7
50 US-08-767-993-10
51 ; Sequence 10, Application US/08767993
52 Patent No. 6010885
53 GENERAL INFORMATION:
54 APPLICANT: TURNER, George J.
55 APPLICANT: BETLACH, Mary C.
56 TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS POLYPEPTIDES
57 TITLE OF INVENTION: IN HALOBACTERIA
58 NUMBER OF SEQUENCES: 15
59 CORRESPONDENCE ADDRESS:
60 ADDRESSEE: Walter H. Dregler
61 STREET: 4 Embarcadero Center, Suite 3400
62 CITY: San Francisco
63 STATE: California
64 COUNTRY: USA
65 ZIP: 94111
66 COMPUTER READABLE FORM:
67 MEDIUM TYPE: Floppy disk
68 COMPUTER: IBM PC compatible
69 OPERATING SYSTEM: PC-DOS/MS-DOS
70 SOFTWARE: PatentIn Release #1.0, Version #1.25
```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,993
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-57666/WMD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1848 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: 376..414
OTHER INFORMATION: /note="Bacteriorhodopsin
OTHER INFORMATION: pre-sequence."
FEATURE:
NAME/KEY: terminator
LOCATION: 1756..1758
OTHER INFORMATION: /note="Bacteriorhodopsin stop
OTHER INFORMATION: codon."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 517..591
OTHER INFORMATION: /note="Helix I of rat serotonin
OTHER INFORMATION: receptor protein (Type Ic)."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 625..690
OTHER INFORMATION: /note="Helix II of rat serotonin
OTHER INFORMATION: receptor protein (Type Ic)."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 736..807
OTHER INFORMATION: /note="Helix III of rat serotonin
OTHER INFORMATION: receptor protein (Type Ic)."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 868..939
OTHER INFORMATION: /note="Helix IV of rat serotonin
OTHER INFORMATION: receptor protein (Type Ic)."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 997..1059
OTHER INFORMATION: /note="Helix V of rat serotonin
OTHER INFORMATION: receptor protein (Type Ic)."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1297..1362
OTHER INFORMATION: /note="Helix VI of rat serotonin
OTHER INFORMATION: receptor protein (Type Ic)."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1411..1476
OTHER INFORMATION: /note="Helix VII of rat serotonin
OTHER INFORMATION: receptor protein (Type Ic)."
FEATURE:
NAME/KEY: mutation
LOCATION: replace(213,"")
OTHER INFORMATION: /note="G to A mutation removes
OTHER INFORMATION: ALWNI restriction site."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1732..1734
OTHER INFORMATION: /note="Codon encoding the
OTHER INFORMATION: C-terminal amino acid of the rat serotonin

```

```
OTHER INFORMATION: receptor protein (Type 1c).
FEATURE:
  NAME/KEY: misc_signal
  LOCATION: 374
  OTHER INFORMATION: /note="RNA start site."
FEATURE:
  NAME/KEY: CDS
  LOCATION: 376..1734
FEATURE:
  NAME/KEY: terminator
  LOCATION: 1735..1737
  OTHER INFORMATION: /note="serotonin stop codon."
FEATURE:
  NAME/KEY: repeat_region
  LOCATION: 436..462
  OTHER INFORMATION: /note="sequence encoding
Patent No. 6010885
OTHER INFORMATION: polypaspartic acid."
FEATURE:
  NAME/KEY: mutation
  LOCATION: replace(1755, "")
  OTHER INFORMATION: /note="C to T mutation removes
  OTHER INFORMATION: AlwNI restriction site."
US-08-767-993-10

Query Match
Best Local Similarity 5.3%; Score 34.6; DB 3; Length 1848;
Best Local Similarity 52.4%; Pred. No. 0.15;
Matches 76; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

OY 11 CCGAGGCGGTGCTGCAGAGAGACACCTAATTATGATTCCTCAGAGAGAGACT 70
DB 1115 CCGAGAGGAGACTGGCTAATATGAGCCTGACCTTCTGACGCTGCTGCAGAGAAATG 1174
OY 71 GTAATATATGCGCAACCCCTAGAGAGATATATACAGAGAAATTCCTAGACAGACAT 130
DB 1175 GTGGTGAGAGAGAGAGAGAGCGTCCGAACCCCTAATCCAGATCAGAAACACGCTCGAAGAGAA 1234
OY 131 ACAACAGCTGTGCCAGACTCTGCTT 155
DB 1235 AAGAAAAGCGTCCCGAGAGGACCAT 1259

RESULT 8
US-09-032-742-3
Sequence 3, Application US/09032742
Patent No. 6255089
GENERAL INFORMATION:
  APPLICANT: Teittler, Milt
  APPLICANT: Herrick-Davis, Katharine
  TITLE OF INVENTION: Constitutively Activated Serotonin
  NUMBER OF SEQUENCES: 25
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Laurence Weinberger
  STREET: 882 S. Malack Street, Suite 103
  CITY: West Chester
  STATE: PA
  COUNTRY: USA
  ZIP: 19380-0053
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/032,742
  FILING DATE: 27-FEB-1998
  CLASSIFICATION: 536
  ATTORNEY/AGENT INFORMATION:
  NAME: Weinberger, Laurence
  REGISTRATION NUMBER: 27,965
```

```
REFERENCE/DOCKET NUMBER: 3086-4
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (610) 431-1703
  TELEFAX: (610) 431-4181
  INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 2246 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
US-09-032-742-3

Query Match
Best Local Similarity 5.3%; Score 34.6; DB 3; Length 2246;
Best Local Similarity 52.4%; Pred. No. 0.16;
Matches 76; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

OY 11 CCGAGGCGGTGCTGCAGAGAGACACCTAATTATGATTCCTCAGAGAGAGACT 70
DB 1448 CCGAGAGGAGACTGGCTAATATGAGCCTGACCTTCTGACGCTGCTGCAGAGAAATG 1507
OY 71 GTAATATATGCGCAACCCCTAGAGAGATATATACAGAGAAATTCCTAGACAGACAT 130
DB 1508 GTGGTGAGAGAGAGAGAGCGTCCGAACCCCTAATCCAGATCAGAAACACGCTCGAAGAGAA 1567
OY 131 ACAACAGCTGTGCCAGACTCTGCTT 155
DB 1568 AAGAAAAGCGTCCCGAGAGGACCAT 1592

RESULT 9
US-09-032-742-21
Sequence 21, Application US/09032742
Patent No. 6255089
GENERAL INFORMATION:
  APPLICANT: Teittler, Milt
  APPLICANT: Herrick-Davis, Katharine
  TITLE OF INVENTION: Constitutively Activated Serotonin
  NUMBER OF SEQUENCES: 25
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Laurence Weinberger
  STREET: 882 S. Malack Street, Suite 103
  CITY: West Chester
  STATE: PA
  COUNTRY: USA
  ZIP: 19380-0053
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/032,742
  FILING DATE: 27-FEB-1998
  CLASSIFICATION: 536
  ATTORNEY/AGENT INFORMATION:
  NAME: Weinberger, Laurence
  REGISTRATION NUMBER: 27,965
  REFERENCE/DOCKET NUMBER: 3086-4
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (610) 431-1703
  TELEFAX: (610) 431-4181
  INFORMATION FOR SEQ ID NO: 21:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 2246 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
US-09-032-742-21
```

Query Match 5.3%; Score 34.6; DB 3; Length 2246;
Best Local Similarity 52.4%; Pred. No. 0.16;
Matches 76; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

11 CCGAGGGGCTGCTCAAGAGAGGACCTTATGAAATTCCTCAGAGAGAGAGACT 70
1448 CCGAGGAGGAACTGCTTAATGAGCCTGAACTTCTGACTGCTGCAAGAGATG 1507

71 GTAATAATGGCAACCCCTAGAAAGATATACAGAGAAATTCATTAGACAGACAT 130
1508 GTGGTAGAGAGAGAGAGAGCTCCGAACCTTAATCCAGATCAGAAACCAAGCTGGAAGAAGA 1567

131 ACAACAGCTGTGCCAGACTCTGCTT 155
1568 AAGAAAGCGTCCAGAGGACACAT 1592

RESULT 10
US-09-032-742-22
; Sequence 22, Application US/09032742
; Patent No. 6255089
; GENERAL INFORMATION:
; APPLICANT: Teitler, Milt
; APPLICANT: Herrick-Davis, Katharine
; APPLICANT: Egan, Christina C.
; TITLE OF INVENTION: Constitutively Activated Serotonin
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Laurence Weinberger
; STREET: 882 S. Malack Street, Suite 103
; CITY: P.O. Box 1663
; STATE: PA
; COUNTRY: USA
; ZIP: 19380-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,742
; FILING DATE: 27-FEB-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Weinberger, Laurence
; REGISTRATION NUMBER: 27,965
; REFERENCE/DOCKET NUMBER: 3086-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 431-1703
; TELEFAX: (610) 431-4181
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2246 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-032-742-22

Query Match 5.3%; Score 34.6; DB 3; Length 2246;
Best Local Similarity 52.4%; Pred. No. 0.16;
Matches 76; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

11 CCGAGGGGCTGCTCAAGAGAGGACCTTATGAAATTCCTCAGAGAGAGAGACT 70
1448 CCGAGGAGGAACTGCTTAATGAGCCTGAACTTCTGACTGCTGCAAGAGATG 1507

71 GTAATAATGGCAACCCCTAGAAAGATATACAGAGAAATTCATTAGACAGACAT 130
1508 GTGGTAGAGAGAGAGAGAGCTCCGAACCTTAATCCAGATCAGAAACCAAGCTGGAAGAAGA 1567

131 ACAACAGCTGTGCCAGACTCTGCTT 155
1568 AAGAAAGCGTCCAGAGGACACAT 1592

RESULT 11
US-09-032-742-24
; Sequence 24, Application US/09032742
; Patent No. 6255089
; GENERAL INFORMATION:
; APPLICANT: Teitler, Milt
; APPLICANT: Herrick-Davis, Katharine
; APPLICANT: Egan, Christina C.
; TITLE OF INVENTION: Constitutively Activated Serotonin
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Laurence Weinberger
; STREET: 882 S. Malack Street, Suite 103
; CITY: P.O. Box 1663
; STATE: PA
; COUNTRY: USA
; ZIP: 19380-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,742
; FILING DATE: 27-FEB-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Weinberger, Laurence
; REGISTRATION NUMBER: 27,965
; REFERENCE/DOCKET NUMBER: 3086-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 431-1703
; TELEFAX: (610) 431-4181
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2246 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-032-742-24

Query Match 5.3%; Score 34.6; DB 3; Length 2246;
Best Local Similarity 52.4%; Pred. No. 0.16;
Matches 76; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

11 CCGAGGGGCTGCTCAAGAGAGGACCTTATGAAATTCCTCAGAGAGAGAGACT 70
1448 CCGAGGAGGAACTGCTTAATGAGCCTGAACTTCTGACTGCTGCAAGAGATG 1507

71 GTAATAATGGCAACCCCTAGAAAGATATACAGAGAAATTCATTAGACAGACAT 130
1508 GTGGTAGAGAGAGAGAGAGCTCCGAACCTTAATCCAGATCAGAAACCAAGCTGGAAGAAGA 1567

131 ACAACAGCTGTGCCAGACTCTGCTT 155
1568 AAGAAAGCGTCCAGAGGACACAT 1592

RESULT 12
US-09-032-742-25
; Sequence 25, Application US/09032742
; Patent No. 6255089
; GENERAL INFORMATION:
; APPLICANT: Teitler, Milt

```

; APPLICANT: Herrick-Davis, Katharine
; APPLICANT: Egan, Christina C.
; TITLE OF INVENTION: Constitutively Activated Serotonin
; TITLE OF INVENTION: Receptors
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Laurence Weinberger
; STREET: 882 S. Mallick Street, Suite 103
; CITY: West Chester
; STATE: PA
; COUNTRY: USA
; ZIP: 19380-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,742
; FILING DATE: 27-FEB-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Weinberger, Laurence
; REGISTRATION NUMBER: 27,965
; REFERENCE/DOCKET NUMBER: 3086-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 431-1703
; TELEFAX: (610) 431-4181
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2246 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-032-742-25

Query Match
Best Local Similarity 5.3%; Score 34.6; DB 3; Length 2246;
Matches 76; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 11 CCGAGCGGCTGCTGCAGAGAGAGCACTCAAGTTTATGATTCCTCAGAGAGAGAACT 70
DB 1448 CCGAGGAGAACTGCTATATATGACCTGAACTTCTGAACTGCTGCAAGAAAG 1507
QY 71 GTAATAATGGCGAACCCCTAGAGATAATACAGAGAAATTCACCTTACAGACAT 130
DB 1508 GTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1567
QY 131 ACACAGCTGTGCGCACTCTGCTT 155
DB 1568 AAGAAAGGCTCCAGAGGACCAT 1592

RESULT 13
US-09-134-001C-2805
; Sequence 2805, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 1998-08-13
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: US 60/055,779
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2805
; LENGTH: 660
```

```

; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-2805

Query Match
Best Local Similarity 4.9%; Score 32; DB 4; Length 660;
Matches 83; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 59 AGAGAGAGAGCTGTATATATGCGCAACCCCTAGAGAGATATACAGAGAGAACTTAC 118
DB 454 AGATTACATATTATTCACCAAGAACTTCTTTTCAACCAATATCAACAGCTCAATCAT 513
QY 119 TTAGACAGACATACACAGCTGTGCGCAGACTGCTTAAACCAAGAAACAGATGTAG 178
DB 514 TTACTACACCAAGATTAAGCAATACAGATGCTTTGCAAGTAAAGAAATGAATTGTG 573
QY 179 CAAGCAGCTGTATGAAGAGTGAATTTGTGCGCAACCAAACTTG 226
DB 574 CAACATGCTTAAAGATACGTGAATATGATCTCAAAAACAAATTTG 621

RESULT 14
US-09-357-206A-8/C
; Sequence 8, Application US/09357206A
; Patent No. 6372962
; GENERAL INFORMATION:
; APPLICANT: Dinesh-Kumar, S.
; APPLICANT: Baker, Barbara
; TITLE OF INVENTION: Pathogen Resistance in Plants using cDNA-N/Intron Constructs
; FILE REFERENCE: 042250/191805 (5830-5)
; CURRENT APPLICATION NUMBER: US/09/357,206A
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 60/093,494
; PRIOR FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8
; LENGTH: 4281
; TYPE: DNA
; ORGANISM: Nicotiana glutinosa
; US-09-357-206A-8

Query Match
Best Local Similarity 4.8%; Score 31.6; DB 4; Length 4281;
Matches 52; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 279 CATGAAAAGAAAAGAACTGTGTCAATATTGAGCGAGTGTGAGAGTCAATCA 338
DB 4265 CTCTGAAAAGAAATAGAACTGTATGTGAAAAATTTGTGATGTGTAAGAAATTAAG 4206
QY 339 ACTGAATTTGTGAACATCTATAT 364
DB 4205 ATGATATTTTCAACAATTTTATAT 4180

RESULT 15
US-09-149-476-288/C
; Sequence 288, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
```

EARLIER APPLICATION NUMBER:	60/040,656
EARLIER FILING DATE:	1997-03-07
EARLIER APPLICATION NUMBER:	60/040,334
EARLIER FILING DATE:	1997-03-07
EARLIER APPLICATION NUMBER:	60/040,336
EARLIER FILING DATE:	1997-03-07
EARLIER APPLICATION NUMBER:	60/040,163
EARLIER FILING DATE:	1997-03-07
EARLIER APPLICATION NUMBER:	60/047,600
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,615
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,597
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,502
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,633
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,583
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,617
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,618
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,503
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,592
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,581
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,584
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,500
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,587
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,492
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,588
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,613
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,582
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,601
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/043,560
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,568
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,314
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,565
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,311
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,671
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,674
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,669
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,312
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,313
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,672

[illegible]

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 05:08:13 : Search time 506.085 Seconds

(without alignments)
8961.061 Million cell updates/sec

Title: US-10-023-530-3

Perfect score: 1680
Sequence: 1 ccggggcgggtgttggcggc.....ccaaaaaaaaaaaaaaaaa 1680

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database : N_Geneseq_10Jun03.*

```
1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1680	100.0	1680	24	ABK86904
2	1602.6	95.4	1692	24	ABSS5576
3	1456.6	86.7	1873	24	ABSS5574
4	1455	86.6	1873	24	ABSS5591
5	1455	86.6	1873	24	ABSS5592
6	1455	86.6	1873	24	ABSS5593
7	1455	86.6	1873	24	ABSS5594
8	1445.6	86.0	1664	24	ABSS5575

9	811.4	48.3	813	24	ABK85817	cDNA encoding huma
10	415.2	24.7	640	21	AAZ80552	Human colon cancer
11	368.8	22.0	381	22	AAZ8571	Novel human diagno
12	240.2	14.3	421	25	ABX42018	Bovine EST associa
13	236.8	14.1	3144	21	AAA27132	Human inflammation
14	236.8	14.1	3144	25	ABX12605	cDNA encoding huma
15	234.4	14.0	303	24	ABK93006	cDNA encoding huma
16	221.2	13.2	3018	20	AAZ25347	Ras binding protei
17	153.8	9.2	760	24	ABQ36586	Oligonucleotide fo
18	153.8	9.2	760	24	ABQ36587	Oligonucleotide fo
19	131	7.8	3030	24	ABK70366	Human bone remodel
20	123.2	7.3	420	22	AAI10131	Human breast cancer
21	123	7.3	403	22	AAI19711	Human breast cancer
22	118.8	7.1	524	23	ABV15836	Human prostate exp
23	118.8	7.1	556	23	ABV30142	Human prostate exp
24	118.8	7.1	556	23	ABV30326	Human prostate exp
25	118.8	7.1	713	23	ABV45636	Human prostate exp
26	118.8	7.1	713	23	ABV45873	Human prostate exp
27	117.6	7.0	760	24	ABQ36588	Oligonucleotide fo
28	117.6	7.0	760	24	ABQ36589	Oligonucleotide fo
29	106.4	6.3	441	23	ABV16075	Human prostate exp
30	96	5.7	356	25	ABX44203	Human EST associa
31	94.8	5.6	239	21	AAA52654	Eosinophil activat
32	62.4	3.7	510	25	ABX12607	Human Ras associat
33	60	3.6	60	24	ABN42558	Human spliced tran
34	56.4	3.4	401	22	AAI85435	Human polynucleoti
35	44.2	2.6	3229	22	AAK82155	Human immune/haema
36	44.2	2.6	6327	24	ABT10150	Human breast cancer
37	41.4	2.5	135638	25	ABX34289	S. atrocolivaceus I
38	39	2.3	50	22	AAI31433	Human SNP oligonuc
39	38.2	2.3	2000	8	AAV71065	Gene encoding Plas
40	37.8	2.2	1484	23	AAZ88098	DNA encoding novel
41	37.6	2.2	1449	23	ABL10349	Drosophila melanog
42	37.6	2.2	1625	23	ABL20863	Drosophila melanog
43	37.6	2.2	2885	23	ABL19562	Drosophila melanog
44	37.6	2.2	4886	23	ABL10348	Drosophila melanog
45	37.6	2.2	4889	23	ABL20862	Drosophila melanog

ALIGNMENTS

RESULT 1	
ID	ABK86904 standard; DNA; 1680 BP.
ABK86904	
AC	ABK86904;
DT	24-SEP-2002 (first entry)
XX	Human Rassf1 prey gene sequence.
DE	
XX	Human; beta Tcrp; bTcrp; protein-protein interaction complex; Ras SFL;
KW	drug screening; selected interacting domain; STD; tumour; gene therapy;
KW	prey protein; cytosolic; gene; ds.
XX	
OS	Homo sapiens.
XX	
FT	key
FT	Location/Qualifiers
FT	59.871
FT	/tag a
FT	/product- "Human Rassf1 protein"
PN	W0200250261-A2.
XX	
PD	27-JUN-2002.
XX	
PF	18-DEC-2001; 2001WO-EP15414.
XX	
PR	18-DEC-2000; 2000US-256276P.
XX	
PA	(HYBR-) HYBRIGENICS.
PA	(INRM) INST NAT SANTE & RECH MEDICALE.

XX Legrain P, Benarous R, Blot G, Lassot I;
 XX WPI: 2002-508795/54.
 DR P-PSDB: AAU98088.
 XX
 PT Protein-protein complexes for screening drugs or agents that modulate
 PT interaction of proteins, e.g. for identifying the Selected Interacting
 PT Domains (SID), comprises interaction between beta-Trip and Ras Sfl -
 XX
 PS Claim 2; Page 47; 84pp: English.

CC The present invention relates to a new complex of protein-protein
 CC interaction between betatrip (not defined in specification) and Ras Sfl.
 CC The protein-protein complex of the invention is useful for screening
 CC drugs or agents that modulate interaction of proteins. In particular,
 CC the protein complex is useful for identifying the Selected Interacting
 CC Domains (SID). The modulating compounds detected can be used for
 CC treating tumours. The polynucleotides encoding the protein complex may
 CC be used in gene therapy. The present nucleic acid sequence encodes the
 CC human RasSfl protein that was used in the methods of the invention as
 CC a prey protein.
 XX

Sequence 1680 BP: 372 A; 433 C; 522 G; 353 T; 0 other:

Query Match 100.0%; Score 1680; DB 24; Length 1680;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1680; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGGGGGGCTGTGGGGGCTGACGAGCGGAGAGCTGGGGGAGCGGGGCTAGCGCTAT 60
 DB 1 CCGGGGGGCTGTGGGGGCTGACGAGCGGAGAGCTGGGGGAGCGGGGCTAGCGCTAT 60
 OY 61 GGGGAGGCGGAGGCGGCTCTTTCGAATGACCTGAGCAGCAGCAGCAGTGGCTA 120
 DB 61 GGGGAGGCGGAGGCGGCTCTTTCGAATGACCTGAGCAGCAGCAGCAGTGGCTA 120
 OY 121 CTGAGCCCAAGAGAGCTGCGACTGCGAGCTGAGCAGTCTTCAACCGGCTAACCTGCT 180
 DB 121 CTGAGCCCAAGAGAGCTGCGACTGCGAGCTGAGCAGTCTTCAACCGGCTAACCTGCT 180
 OY 181 AGCTGCGAGCGGCGGCGGAGCAGCAGCAGCTGTGGAGTGGGAGCAGCTGACCTTTC 240
 DB 181 AGCTGCGAGCGGCGGCGGAGCAGCAGCAGCTGTGGAGTGGGAGCAGCTGACCTTTC 240
 OY 241 TCAAGCTGAGATTGAGCAGAGATCAAGAGTACATGCCAGATCAACAGCAACCTCTT 300
 DB 241 TCAAGCTGAGATTGAGCAGAGATCAAGAGTACATGCCAGATCAACAGCAACCTCTT 300
 OY 301 CATAGCTTGAACAAGAGCGTCTTACACAGCTTCAAGGTTCAAGCTGAAGCTGGT 360
 DB 301 CATAGCTTGAACAAGAGCGTCTTACACAGCTTCAAGGTTCAAGCTGAAGCTGGT 360
 OY 361 GCGGCGCTGTCTGTGCGCTCCAGCAAGAACCCACCTCTTGGAGAGTGGCGGCGGG 420
 DB 361 GCGGCGCTGTCTGTGCGCTCCAGCAAGAACCCACCTCTTGGAGAGTGGCGGCGGG 420
 OY 421 CCCAGGAGCGGCGCAAGTGTCAAGCGCGGCACTTCTTAACTTGCCTCAAGATGCTGT 480
 DB 421 CCCAGGAGCGGCGCAAGTGTCAAGCGCGGCACTTCTTAACTTGCCTCAAGATGCTGT 480
 OY 481 CAAGCAGCTGATGTGCTGTACGACAGGCGCAGTGAAGTCAATTGAGCGGCTGTCGG 540
 DB 481 CAAGCAGCTGATGTGCTGTACGACAGGCGCAGTGAAGTCAATTGAGCGGCTGTCGG 540
 OY 541 AAAGTTCTGTGTGATGATGACCCCGCAAGTTGCACTCTTAAAGGCGCTGAGCGCA 600
 DB 541 AAAGTTCTGTGTGATGATGACCCCGCAAGTTGCACTCTTAAAGGCGCTGAGCGCA 600
 OY 601 CCGCCAAAGTACTTGGGGAAGCTGTGGATGATGAGCAGCCCTGGCGCTGCGGCTCT 660
 DB 601 CCGCCAAAGTACTTGGGGAAGCTGTGGATGATGAGCAGCCCTGGCGCTGCGGCTCT 660

OY 661 GCGAGGCGCCAGTAGACAAAGGCCCTGAGCTTTGTCTGTAAGGAAATGACTCTGGGAGCT 720
 DB 661 GCGAGGCGCCAGTAGACAAAGGCCCTGAGCTTTGTCTGTAAGGAAATGACTCTGGGAGCT 720
 OY 721 GAAGTGGAGCGCTTACAGATGCTGTAAGTCAATTAAGTCTTCTAGTATCTCTGACGGGA 780
 DB 721 GAAGTGGAGCGCTTACAGATGCTGTAAGTCAATTAAGTCTTCTAGTATCTCTGACGGGA 780
 OY 781 GGAGGAGAGCAGCTCCGCGAGATCTGACAGATCTCTTAATGCGCGCAGGAATCA 840
 DB 781 GGAGGAGAGCAGCTCCGCGAGATCTGACAGATCTCTTAATGCGCGCAGGAATCA 840
 OY 841 AGAGCCCTGACAGCGCTCCGCGAGATCTGACAGATCTCTTAATGCGCGCAGGAATCA 900
 DB 841 AGAGCCCTGACAGCGCTCCGCGAGATCTGACAGATCTCTTAATGCGCGCAGGAATCA 900
 OY 901 AGCAGGAGCGGCGCAAGTGGCGGCTGAGATGAGCAGGCGCAGTGGCGCTGCAAT 960
 DB 901 AGCAGGAGCGGCGCAAGTGGCGGCTGAGATGAGCAGGCGCAGTGGCGCTGCAAT 960
 OY 961 GAGTGTGATGAGAGCGCTCTGCTGTGGGGAATGAGCCAGAAACAGGAAATGAGT 1020
 DB 961 GAGTGTGATGAGAGCGCTCTGCTGTGGGGAATGAGCCAGAAACAGGAAATGAGT 1020
 OY 1021 TGCTCCCTGTGTCACCTAGTGGGTGAGCCAGTATGAGCTTGCACCCCTGCTCAT 1080
 DB 1021 TGCTCCCTGTGTCACCTAGTGGGTGAGCCAGTATGAGCTTGCACCCCTGCTCAT 1080
 OY 1081 TACTGGGCGCTAAGTGGCGCAGGCGCTGCGCTGAGAAAGTCTGCAAGGCTGAGAGAGT 1140
 DB 1081 TACTGGGCGCTAAGTGGCGCAGGCGCTGCGCTGAGAAAGTCTGCAAGGCTGAGAGAGT 1140
 OY 1141 GGTGAGAGCAAGATCTCTCAATTTTGTCTGAAAGTGAATCTTGGAGACCTGCA 1200
 DB 1141 GGTGAGAGCAAGATCTCTCAATTTTGTCTGAAAGTGAATCTTGGAGACCTGCA 1200
 OY 1201 AACAGAACAGGCTATGTTTTCAGGCGGTGACGCGCTCATATATAGAGAAAGTTTGA 1260
 DB 1201 AACAGAACAGGCTATGTTTTCAGGCGGTGACGCGCTCATATATAGAGAAAGTTTGA 1260
 OY 1261 TCTTGAATGTGCTCAGAGATATCTTATCAGACTTAAGGCTGGGCTCGAATAAGGC 1320
 DB 1261 TCTTGAATGTGCTCAGAGATATCTTATCAGACTTAAGGCTGGGCTCGAATAAGGC 1320
 OY 1321 AGGCAATGAGAGAGTCTTGGTCTCTTACAGTGCACATCTCAGACACCTGAGG 1380
 DB 1321 AGGCAATGAGAGAGTCTTGGTCTCTTACAGTGCACATCTCAGACACCTGAGG 1380
 OY 1381 TCAGGAGAGTGTGCTCAGACTACAGATGTCCTTAATGCTTAATGAGAGAGATGTC 1440
 DB 1381 TCAGGAGAGTGTGCTCAGACTACAGATGTCCTTAATGCTTAATGAGAGAGATGTC 1440
 OY 1441 CCTGGGCGAGGCTGTGTGAATGTGGGCACTGGCCAGGTTCAATTAATTTGGCTAAT 1500
 DB 1441 CCTGGGCGAGGCTGTGTGAATGTGGGCACTGGCCAGGTTCAATTAATTTGGCTAAT 1500
 OY 1501 CAAAGCCAGGCTCTCTCTCAGCTAGGTTTATGAAGTGCCTAATGTAATGTGT 1560
 DB 1501 CAAAGCCAGGCTCTCTCTCAGCTAGGTTTATGAAGTGCCTAATGTAATGTGT 1560
 OY 1561 GGTGGCTCAGCTGAATGCTCTCTCTGAGGGAAGGCTGGGAGTGAAGTATCATCAGG 1620
 DB 1561 GGTGGCTCAGCTGAATGCTCTCTCTGAGGGAAGGCTGGGAGTGAAGTATCATCAGG 1620
 OY 1621 CCTGGGCTGAGAAATTTGGCTCAATAAAGTTCAAGATCCAAAAA 1680
 DB 1621 CCTGGGCTGAGAAATTTGGCTCAATAAAGTTCAAGATCCAAAAA 1680

RESULT 2
 ABS5576
 ID ABS5576 standard; cDNA: 1692 BP.
 XX

AC ABSS5576;
XX 19-DEC-2002 (first entry)
XX Human cDNA encoding tumour suppressor RASSFL1.C.
DE
XX
XX Human; ss; gene; tumour suppressor; RASSFL1.C; cancer; breast cancer;
KM DNA methylation; lung cancer; kidney cancer; ovarian cancer;
KM head and neck cancer; melanoma; chromosome 3p21.3.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 12..824
XX /tag="a
XX /product="RASSFL1.C"
XX
XX US2002098530-A1.
XX
XX 25-JUL-2002.
XX
XX 30-MAR-2001; 2001US-0821803.
XX
XX 30-MAR-2000; 2000US-193268P.
XX
XX (CITY) CITY OF HOPE.
XX
XX Pfeiffer GP, Dammann R;
XX
XX MPI: 2002-690479/74.
XX P-PSDB; ABG71309.
XX
XX Novel tumor suppressor gene, termed RASSFL1, useful for the diagnosis of
XX predisposition to cancer by analyzing its methylation status,
XX heterozygosity or mutation
XX
XX
XX Claim 2: Page 32-34; 57pp; English.
XX
XX The invention relates to an isolated tumour suppressor gene coding for
XX splice variant RASSFL1.A, RASSFL1.B or RASSFL1.C protein or its complement,
XX or a DNA molecule which hybridises under stringent conditions to them.
XX Also included are naturally occurring mutants of RASSFL1.A, detecting (M1)
XX a methylated RASSFL1 gene, non-expressed RASSFL1 gene or an alteration in
XX RASSFL1 where the methylation, non-expression or alteration is associated
XX with cancer in a human, by analysing an RASSFL1 gene or an RASSFL1 gene
XX expression product from a tissue or body fluid of the human;
XX administering RASSFL1 agonists to treat cancer, a RASSFL1 non-human
XX transgenic animal, a cell line from the transgenic animal, and
XX screening for cancer therapeutics/drug candidates useful in treating
XX cancer resulting from a methylated or a mutation in RASSFL1.
XX (M1) is useful for detecting methylated RASSFL1 gene, which is
XX useful for determining whether a human subject has or is at risk for
XX developing cancer. The method involves detecting the methylation or
XX non-expression of the gene or the presence or absence of a genetic
XX polymorphism as in the RASSFL1 gene of the subject, where the
XX methylation or non-expression or the presence of the genetic
XX polymorphism identifies a subject that has or is at risk for developing
XX cancer. The mutants are useful for screening for drug candidates useful
XX in treating cancer resulting from the RASSFL1 gene. Analysis of the RASSFL1
XX gene is useful in the diagnosis of predisposition to cancer, including
XX lung, breast, kidney, ovarian, head and neck cancer and melanoma. The
XX association between the RASSFL1 gene and cancer permits the early
XX pre-symptomatic screening of individuals to identify those at risk for
XX developing cancer. RASSFL1 protein is useful for identifying agonists of
XX the biological function of an RASSFL1 protein. RASSFL1, its encoding
XX nucleic acids, antibodies and compounds identified by the screening
XX assays are useful for treating cancer. The gene for RASSFL1 is located
XX on chromosome 3p21.3. The present sequence encodes the RASSFL1 splice
XX variant RASSFL1.C.
XX
XX Sequence 1692 BP; 424 A; 423 C; 498 G; 347 T; 0 other;
XX
XX Query Match 95.4%; Score 1602.6; DB 24; Length 1692;

Best Local Similarity 99.6%; Pred. No. 0;
Matches 1628; Conservative 0; Mismatches 4; Indels 3; Gaps 2;
QY 48 CCGGTACGGCTATGGGCGAGGGGAGGCGGCTCTTTCGAATAGACCTGGAGCAGACA 107
DB 1 CCGGTACGGCTATGGGCGAGGGGAGGCGGCTCTTTCGAATAGACCTGGAGCAGACA 60
QY 108 CGAGCAGTGGCTACTGACCCCAAGAGACTCGGAGCTCGAGCTGAGCAGTACTTCCAGC 167
DB 61 CGAGCAGTGGCTACTGACCCCAAGAGACTCGGAGCTCGAGCTGAGCAGTACTTCCAGC 120
QY 168 CCGGAACCTCGCTAGCTCCAGGCGCGCCGGGACCCAGACGAGCCTGTGAGTGGAGA 227
DB 121 CCGGAACCTCGCTAGCTCCAGGCGCGCCGGGACCCAGACGAGCCTGTGAGTGGAGA 180
QY 228 CAGCTGACCTTCTCAGGCTGAGATGAGCAGAGATTCAGAGGATCAATGGCCCATATCA 287
DB 181 CAGCTGACCTTCTCAGGCTGAGATGAGCAGAGATTCAGAGGATCAATGGCCCATATCA 240
QY 288 ACAGCAACCTCTTCATGAGCTTGAAACAGAGCGTTCCTTACAGGCTTCATCAAGTTC 347
DB 241 ACAGCAACCTCTTCATGAGCTTGAAACAGAGCGTTCCTTACAGGCTTCATCAAGTTC 300
QY 348 AGCTGAGCTGGTGGCCCTGTCTGTGCTGCTCCACGACAGAACCCCTCTTCCAGC 407
DB 301 AGCTGAGCTGGTGGCCCTGTCTGTGCTCCACGACAGAACCCCTCTTCCAGC 360
QY 408 ATGCCCCGGGGGGCCAGAGCGGGGACAAAGTGTACGGCGCCGCACTTCTTACTCTG 467
DB 361 ATGCCCCGGGGGGCCAGAGCGGGGACAAAGTGTACGGCGCCGCACTTCTTACTCTG 420
QY 468 CCAAGAGTCTGTCAAGCAGCTGATGCTCTGTCAAGCAGCAAGGCGACGTGAAGTATG 527
DB 421 CCAAGAGTCTGTCAAGCAGCTGATGCTCTGTCAAGCAGCAAGGCGACGTGAAGTATG 480
QY 528 AGGCGCTGCTGGCAAGTCTTGTGTGTGTGATGATCCCGCAAGTGTGACTTGTGAC 587
DB 481 AGGCGCTGCTGGCAAGTCTTGTGTGTGTGATGATCCCGCAAGTGTGACTTGTGAC 540
QY 588 GGGCTGAGGCTACGGGCGCAAGTACTTGGGAGGAGTGTGATGATGAGGCGCCCTG 647
DB 541 GGGCTGAGGCTACGGGCGCAAGTACTTGGGAGGAGTGTGATGATGAGGCGCCCTG 600
QY 648 GGGTGGGCTCTCGGAGGCGCCAGTACAAAGGCGCTGAGTGTCTGTAAGGAATG 707
DB 601 GGGTGGGCTCTCGGAGGCGCCAGTACAAAGGCGCTGAGTGTCTGTAAGGAATG 660
QY 708 ACTCTGGGAGGTGAAGTGGAGCGCTTACAGATGCTGAATCAATTAATCTTCACTGA 767
DB 661 ACTCTGGGAGGTGAAGTGGAGCGCTTACAGATGCTGAATCAATTAATCTTCACTGA 720
QY 768 TCGTGGAGGGGAGGAGGAGGACCTCGCCAGATCTCGAAGTACTCTATTTGCC 827
DB 721 TCGTGGAGGGGAGGAGGAGGACCTCGCCAGATCTCGAAGTACTCTATTTGCC 780
QY 828 GCCAGAGATCCAAAGAGGCGCTGACGCGCTGCGCCCTTGGTGGTCACTTTGACCCAG 887
DB 781 GCCAGAGATCCAAAGAGGCGCTGACGCGCTGCGCCCTTGGTGGTCACTTTGACCCAG 840
QY 888 GTGGAAGGACAGACAGCAGCAGCGCCAGTGGCTGCTGTGAGTGTGACAGGCGCAGTG 947
DB 841 GTGGAAGGACAGACAGCAGCAGCGCCAGTGGCTGCTGTGAGTGTGACAGGCGCAGTG 900
QY 948 GGGCGGTGGAAATGATGTGATGAGGAGGCGCCCTTGGTGGGGAATAGGCCAGAGAA 1007
DB 901 GGGCGGTGGAAATGATGTGATGAGGAGGCGCCCTTGGTGGGGAATAGGCCAGAGAA 960
QY 1008 CAGCGAAGTATGCTGCTCTGTGCTACCTATGAGTGTAGCAGAGTATGCTGCTGAC 1067
DB 961 CAGCGAAGTATGCTGCTCTGTGCTACCTATGAGTGTAGCAGAGTATGCTGCTGAC 1020
QY 1068 CCTGTGCTCTATTTACTGAGGCTTGTGAGGCGCAGGCGCTGCTGAGAACCTGCTCAGGC 1127

```

Db 1021 CCTCTGCCCTATTACTGGGCTTAGTGGCCAGGCGTCCCTGGAAGAGTGTCTCCAGGC 1080
Oy 1128 CTGCAGCAGAGTGGTGCAGACAGAGTCTCTCAATTTTGTCTCAGAGTGAATCT 1187
Db 1081 CTGCAGCAGAGTGGTGCAGACAGAGTCTCTCAATTTTGTCTCAGAGTGAATCT 1140
Oy 1188 TGGAGACCTCTCAACAGACAGAGTCTCTCAATTTTGTCTCAGAGTGAATCT 1247
Db 1141 TGGAGACCTCTCAACAGACAGAGTCTCTCAATTTTGTCTCAGAGTGAATCT 1200
Oy 1248 GAAAGGTTTGGATCTTGAATGTGGTCTCAGAGTATCTTTACAGAGTGAAGGTTG 1307
Db 1201 GAAAGGTTTGGATCTTGAATGTGGTCTCAGAGTATCTTTACAGAGTGAAGGTTG 1260
Oy 1308 CTGAGAAATAGGACAGGATAGGAGAGTCTTGGTTTCTCTCAAGTGCCTCTC 1367
Db 1261 CTGAGAAATAGGACAGGATAGGAGAGTCTTGGTTTCTCTCAAGTGCCTCTC 1320
Oy 1368 ACACACCTTGAGTTCAGGAGTCTCTCAAGTGCCTCTCAAGTGCCTCTCA 1427
Db 1321 ACACACCTTGAGTTCAGGAGTCTCTCAAGTGCCTCTCAAGTGCCTCTCA 1380
Oy 1428 TGAGAGAGTCTCTGAGGAGGATCTGTGTAATGTGGGACATGGCCAGGTTCA 1487
Db 1381 TGAGAGAGTCTCTGAGGAGGATCTGTGTAATGTGGGACATGGCCAGGTTCA 1440
Oy 1488 CTATTTTGTATCAAGAGGATCTCTCTCAAGTGTCTTATGAGTGCCTCA 1547
Db 1441 CTATTTTGTATCAAGAGGATCTCTCTCAAGTGTCTTATGAGTGCCTCA 1499
Oy 1548 GTATGTATGTGTGTGGCTCAGCTGATGCTCTCTGTGGGAAAGGTTGGGTCAC 1607
Db 1500 GTATGTATGTGTGTGGCTCAGCTGATGCTCTCTGTGGGAAAGGTTGGGTCAC 1559
Oy 1608 AGTCAATCATCAG--CCTGGGCTGAGAGATGTGCTCAATTAAGATTTCAAGTCCAA 1665
Db 1560 AGTCAATCATCAGGCGCTGGGCGCTGAGAGATGTGCTCAATTAAGATTTCAAGTCCAA 1619
Oy 1666 AAAAAAAAAAAAAA 1680
Db 1620 AAAAAAAAAAAAAA 1634

RESULT 3
ABSS5574
ID ABSS5574 standard; cDNA: 1873 BP.
XX
AC ABSS5574;
XX
DT 19-DEC-2002 (first entry)
XX
DE Human cDNA encoding tumour suppressor RASFL1.A.
XX
KW Human; ss; gene; tumour suppressor; RASFL1.A; cancer; breast cancer;
KW SNP; single nucleotide polymorphism; DNA methylation; lung cancer;
KW kidney cancer; ovarian cancer; head and neck cancer; melanoma;
KW chromosome 3p21.3.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 39..1061
XX FT /tag= a
XX FT /product= "RASFL1.A"
XX FT /replace (99,C)
XX FT /tag= b
XX FT /standard_name= "Single nucleotide polymorphism"
XX
XX US2002098530-A1.
XX
XX 25-JUL-2002.
XX
XX 30-MAR-2001; 2001US-0821803.

```

```

XX 30-MAR-2001; 2000US-193268P.
PR
XX
XX (CITY ) CITY OF HOPE.
PA
XX
XX Pfeiffer GP, Dannmann R;
PI
XX
XX WPI: 2002-690479/74.
DR
XX
XX P-PSDB; ABG71307.
PT
XX
XX Novel tumor suppressor gene, termed RASFL1, useful for the diagnosis of
PT predisposition to cancer by analyzing its methylation status,
PT heterozygosity or mutation
XX
XX
XX Claim 2; Page 28-29; 57pp; English.
XX
XX The invention relates to an isolated tumour suppressor gene coding for
XX splice variant RASFL1.A, RASFL1.B or RASFL1.C protein or its complement,
XX or a DNA molecule which hybridises under stringent conditions to them.
XX Also included are naturally occurring mutants of RASFL1.A, detecting (M1)
XX a methylated RASFL1 gene, non-expressed RASFL1 gene or an alteration in
XX RASFL1 where the methylation, non-expression or alteration is associated
XX with cancer in a human, by analysing an RASFL1 gene or an RASFL1
XX expression product from a tissue or body fluid of the human;
XX administering RASFL1 agonists to treat cancer, a RASFL1 non-human
XX transgenic animal, a cell line from the transgenic animal, and
XX screening for cancer therapeutics/drug candidates useful in treating
XX cancer resulting from a methylated or a mutation in RASFL1.
XX (M1) is useful for detecting methylated RASFL1 gene, which is
XX useful for determining whether a human subject has or is at risk for
XX developing cancer. The method involves detecting the methylation or
XX non-expression of the gene or the presence or absence of a genetic
XX polymorphism as in the RASFL1 gene of the subject, where the
XX methylation or non-expression or the presence of the genetic
XX polymorphism identifies a subject that has or is at risk for developing
XX cancer. The mutants are useful for screening for drug candidates useful
XX in treating cancer resulting from the RASFL1 gene. Analysis of the RASFL1
XX gene is useful in the diagnosis of predisposition to cancer, including
XX lung, breast, kidney, ovarian, head and neck cancer and melanoma. The
XX association between the RASFL1 gene and cancer permits the early
XX presymptomatic screening of individuals to identify those at risk for
XX developing cancer. RASFL1 protein is useful for identifying agonists of
XX the biological function of an RASFL1 protein. RASFL1, its encoding
XX nucleic acids, antibodies and compounds identified by the screening
XX assays are useful for treating cancer. The gene for RASFL1 is located
XX on chromosome 3p21.3. The present sequence encodes the RASFL1 splice
XX variant RASFL1.A.
XX
XX Sequence 1873 BP; 394 A; 516 C; 585 G; 378 T; 0 other;
XX
XX Query Match 86.7%; Score 1456.6; DB 24; Length 1873;
XX Best Local Similarity 98.9%; Pred. No. 0;
XX Matches 1477; Conservative 0; Mismatches 14; Indels 2; Gaps 1;
Oy 190 GCCCGCGCGGACAGCAGCAGCTGTGAGTGGAGACACCTTCTTCAAGTGA 249
Db 380 GCGGAGACAGCAAGCTGAGCAGCTGTGAGTGGAGACACCTTCTTCAAGTGA 439
Oy 250 GATTGAGCAGAGATCAAGAGTACATGCGCAGATCAAGCAAGCAAGCTTCAAGACTT 309
Db 440 GATTGAGCAGAGATCAAGAGTACATGCGCAGATCAAGCAAGCAAGCTTCAAGACTT 499
Oy 310 GAAACAGAGAGGTTCTTACACAGGCTTCAATCAAGGTTGAGTGTGCGCCCTGT 369
Db 500 GAAACAGAGAGGTTCTTACACAGGCTTCAATCAAGGTTGAGTGTGCGCCCTGT 559
Oy 370 CTCTGTGCTCTCCAGCAAGAGCAGCAGCTCTTGCAGAGATGCCGCGGCGCCAGAGC 429
Db 560 CTCTGTGCTCTCCAGCAAGAGCAGCAGCTCTTGCAGAGATGCCGCGGCGCCAGAGC 619
Oy 430 GGGCAGAGTGTCAAGGCGGCGCACTTCTTACCTGCCCAAGAGATCTGTCAAGCACT 489
Db 620 GGGCAGAGTGTCAAGGCGGCGCACTTCTTACCTGCCCAAGAGATCTGTCAAGCACT 679

```

```

OY 490 GCATGCTGCTGACGACAGGCGACGTGAAGTCATGTAGGCCCTGCTCGAAAGTTCTT 549
    |||||
DB 680 ACATGTGCTGCTACGACAGGCGACGTGAAGTCATGTAGGCCCTGCTCGAAAGTTCTT 739
OY 550 GGTGGTGAAGTACCCCGCAAGTTTGCACTCTTTGAGCGCGCTGAGCGCTCAGGCCCACT 609
    |||||
DB 740 GGTGGTGAAGTACCCCGCAAGTTTGCACTCTTTGAGCGCGCTGAGCGCTCAGGCCCACT 799
OY 610 GTACTTTCGGAAGCTGTTGGATGATGAGCAGCCCTGCGGCTGCGGCTCTGCGCAGAGGCC 669
    |||||
DB 800 GTACTTTCGGAAGCTGTTGGATGATGAGCAGCCCTGCGGCTGCGGCTCTGCGCAGAGGCC 859
OY 670 CAGTGACAAAGGCCCTGAGCTTTGCTCTGAGGAAATGACTCTGGGAGGTGAATGGGA 729
    |||||
DB 860 CAGTGACAAAGGCCCTGAGCTTTGCTCTGAGGAAATGACTCTGGGAGGTGAATGGGA 919
OY 730 GGCCTTCAGCAGTCCCTGAACTACATTAATCTTACTATACCTGCAAGCGGAGAGAGAGA 789
    |||||
DB 920 GGCCTTCAGCAGTCCCTGAACTACATTAATCTTACTATACCTGCAAGCGGAGAGAGAGA 979
OY 790 GCACCTCCGCGCAGATCTGCAAGAGTACTCTATTGCGCGCAGAAAGATCCAGAGAGCCCT 849
    |||||
DB 980 GCACCTCCGCGCAGATCTGCAAGAGTACTCTATTGCGCGCAGAAAGATCCAGAGAGCCCT 1039
OY 850 GCACGCGTGGCCCTGCTGGGTGACCTTTGTACCCCGAGGTGGAAAGGACAGACAGCAGCAG 909
    |||||
DB 1040 GCACGCGTGGCCCTGCTGGGTGACCTTTGTACCCCGAGGTGGAAAGGACAGACAGCAGCAG 1099
OY 910 CCGCAGAGTCCGCGCGCTGTGATGTGACAGGCGCAGTGGGCGCTGTGGAATGAGTGTGA 969
    |||||
DB 1100 CCGCAGAGTCCGCGCGCTGTGATGTGACAGGCGCAGTGGGCGCTGTGGAATGAGTGTGA 1159
OY 970 TGGAGGCGCTGCTGCTGGGTGAGGAATGAGCCAGACAGCAGGAATGACTTGTCTCCCTG 1029
    |||||
DB 1160 TGGAGGCGCTGCTGCTGGGTGAGGAATGAGCCAGACAGGAATGACTTGTCTCCCTG 1219
OY 1030 TGTCCACTATGAGGTGTGACAGGATGAGCTCTGCAACCCCTGCTCCTATTACTGGGCC 1089
    |||||
DB 1220 TGTCCACTATGAGGTGTGACAGGATGAGCTCTGCAACCCCTGCTCCTATTACTGGGCC 1279
OY 1090 TTAGTGGGCGCAGGCGCGCTCCAGAAAGTCTCCAGAGCGCTGCAAGCAGAGAGTGTGAGAC 1149
    |||||
DB 1280 TTAGTGGGCGCAGGCGCGCTCCAGAAAGTCTCCAGAGCGCTGCAAGCAGAGAGTGTGAGAC 1339
OY 1150 AGAAGTCTCCTCAATTTTGTCTCAGAAAGTGAATAATCTTGAGAGACCCCTCAACAGACAGA 1209
    |||||
DB 1340 AGAAGTCTCCTCAATTTTGTCTCAGAAAGTGAATAATCTTGAGAGACCCCTCAACAGACAGA 1399
OY 1210 GGGTCATGTTTCAGAGGGGTGACGCGCTCATCTATGAGGAAAGGTTTGGATCTTGAATG 1269
    |||||
DB 1400 GGGTCATGTTTCAGAGGGGTGACGCGCTCATCTATGAGGAAAGGTTTGGATCTTGAATG 1459
OY 1270 TGGTCTCAGAGATATCTTATCAGAGCTAAGGGGGGTGCTCAGAAATGAAGCAGGACTTGA 1329
    |||||
DB 1460 TGGTCTCAGAGATATCTTATCAGAGCTAAGGGGGGTGCTCAGAAATGAAGCAGGACTTGA 1519
OY 1330 GGAAGAGTCTGTTTCTCTACAGTGCCTCACTCCACACACCCCTGAGAGTCAAGAGAT 1389
    |||||
DB 1520 GGAAGAGTCTGTTTCTCTACAGTGCCTCACTCCACACACCCCTGAGAGTCAAGAGAT 1579
OY 1390 GGTGGCTCAGACAGTACAGATGTGCTTAAATGCTTCATATGAGAGAGATGCTCCCTGGGCCA 1449
    |||||
DB 1580 GGTGGCTCAGACAGTACAGATGTGCTTAAATGCTTCATATGAGAGAGATGCTCCCTGGGCCA 1639
OY 1450 GGGTCTGTGTGATGTGGGCGACGCGCGCAGGTTCATACCTTATTCTCTAATCAAAAGCAG 1509
    |||||
DB 1640 GGGTCTGTGTGATGTGGGCGACGCGCGCAGGTTCATACCTTATTCTAATCAAAAGCAG 1699
OY 1510 GGTCTCTCCCTCAGTGTGTTTATGAAAGTGCCTGAATGATATGATGATGATGATGATGATGAT 1569
    |||||
DB 1700 GGTCTCTCCCTCAGTGTGTTTATGAAAGTGCCTGAATGATGATGATGATGATGATGATGATGAT 1759

```

```

OY 1570 ACCTGAATCCTCTCTCTGCGGAAAGGGGTTGGGGTGACAGTCAATCAAG--CTTGGGG 1627
    |||||
DB 1760 ACCTGAATCCTCTCTCTGCGGAAAGGGGTTGGGGTGACAGTCAATCAAGGCGCTGGGGC 1819
OY 1628 CTGAGAGAAATGGCTCAATTAAGATTTCAAGATTCACAAAAAATGAAAAAATGAAAAA 1680
    |||||
DB 1820 CTGAGAGAAATGGCTCAATTAAGATTTCAAGATTCACAAAAAATGAAAAAATGAAAAA 1872

RESULT 4
ABS55591
ID ABS55591 standard; cDNA: 1873 BP.
XX
AC ABS55591;
XX
DT 19-DEC-2002 (first entry)
XX
DE Human cDNA encoding tumour suppressor RASSFLA variant 1.
XX
KW Human; ss; gene; tumour suppressor; RASSFLA; cancer; breast cancer;
KW SNP; single nucleotide polymorphism; DNA methylation; lung cancer;
KW kidney cancer; ovarian cancer; head and neck cancer; melanoma;
KW chromosome 3p21.3.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 39..1061
FT /tag= b
FT /product= "RASSFLA"
FT /replace (99,C)
FT /*tag= b
FT /standard.name= "Single nucleotide polymorphism"
FT /replace (425,C)
FT /*tag= c
XX
PN US2002098530-A1.
XX
PD 25-JUL-2002.
XX
PF 30-MAR-2001; 2001US-0821803.
XX
PR 30-MAR-2000; 2000US-193268P.
XX
PA (CITY ) CITY OF HOPE.
PI Pfeiffer GP, Dammann R;
XX
XX WPI; 2002-690479/74.
XX
XX P-PSDB; ABG71310.
XX
PT Novel tumor suppressor gene, termed RASSFL, useful for the diagnosis of
PT predisposition to cancer by analyzing its methylation status,
PT heterozygosity or mutation
XX
XX
PS Claim 3; Page -: 57pp; English.
XX
XX
XX The invention relates to an isolated tumour suppressor gene coding for
XX splice variant RASSFLA, RASSFLB or RASSFLC protein or its complement,
XX or a DNA molecule which hybridises under stringent conditions to them.
XX Also included are naturally occurring mutants of RASSFLA, detecting (M1)
XX a methylated RASSFL gene, non-expressed RASSFL gene or an alteration in
XX RASSFL where the methylation, non-expression or alteration is associated
XX with cancer in a human, by analysing an RASSFL gene or an RASSFL gene
XX expression product from a tissue or body fluid of the human;
XX administering RASSFL agonists to treat cancer, a RASSFL non-human
XX transgenic animal, a cell line from the transgenic animal, and
XX screening for cancer therapeutics/drug candidates useful in treating
XX cancer resulting from a methylated or a mutation in RASSFL.
XX (M1) is useful for detecting methylated RASSFL gene, which is
XX useful for determining whether a human subject has or is at risk for
XX cancer developing. The method involves detecting the methylation or
XX non-expression of the gene or the presence or absence of a genetic

```


FT	/product= "RASSFL.A"
FT	/replace (99,C)
FT	/tag- b
FT	/standard_name= "Single nucleotide polymorphism"
FT	variation /basepair (442,T)
FT	/*tag- c
XX	
PN	US2002098530-A1.
PX	
PD	25-JUL-2002.
PE	
PF	30-MAR-2001; 2001US-0821803.
PR	30-MAR-2000; 2000US-193268P.
PA	(CITY) CITY OF HOPE.
PI	
PJ	Pfeiffer GP, Dammann R;
PK	
DR	WP1; 2002-690479/74.
DX	P-PsDB; ABG71311.
XX	
PT	Novel tumor suppressor gene, termed RASSFL, useful for the diagnosis of
PT	predisposition to cancer by analyzing its methylation status,
PT	heterozygosity or mutation -
PS	
PS	Claim 3; Page -: 57pp; English.
XX	
CC	The invention relates to an isolated tumour suppressor gene coding for
CC	splice variant RASSFL.A, RASSFL.B or RASSFL.C protein or its complement,
CC	or a DNA molecule which hybridises under stringent conditions to them.
CC	Also included are naturally occurring mutants of RASSFL.A, detecting (M1)
CC	a methylated RASSFL gene, non-expressed RASSFL gene or an alteration in
CC	RASSFL where the methylation, non-expression or alteration is associated
CC	with cancer in a human, by analysing an RASSFL gene or an RASF gene
CC	expression product from a tissue or body fluid of the human;
CC	administering RASSFL agonists to treat cancer, a RASSFL non-human
CC	transgenic animal, a cell line from the transgenic animal, and
CC	screening for cancer therapeutics/drug candidates useful in treating
CC	cancer resulting from a methylated or a mutation in RASSFL.
CC	(M1) is useful for detecting methylated RASSFL gene, which is
CC	useful for determining whether a human subject has or is at risk for
CC	developing cancer. The method involves detecting the methylation or
CC	non-expression of the gene or the presence or absence of a genetic
CC	polymorphism as in the RASSFL gene of the subject, where the
CC	methylation or non-expression or the presence of the genetic
CC	polymorphism identifies a subject that has or is at risk for developing
CC	cancer. The mutants are useful for screening for drug candidates useful
CC	in treating cancer resulting from the RASSFL gene. Analysis of the RASSFL
CC	gene is useful in the diagnosis of predisposition to cancer, including
CC	lung, breast, kidney, ovarian, head and neck cancer and melanoma. The
CC	association between the RASSFL gene and cancer permits the early
CC	presymptomatic screening of individuals to identify those at risk for
CC	developing cancer. RASSFL protein is useful for identifying agonists of
CC	the biological function of an RASSFL protein. RASSFL, its encoding
CC	nucleic acids, antibodies and compounds identified by the screening
CC	assays are useful for treating cancer. The gene for RASSFL is located
CC	on chromosome 3p1.3. The present sequence encodes a natural variant of
CC	RASSFL splice variant RASSFL.A.
CC	Note: The present sequence is not shown in the specification but
CC	was created by the indexer using the information in claim 3 and the
CC	RASSFL.A sequence appearing as AB555574.
XX	
SQ	Sequence 1873 BP: 394 A: 517 C: 585 G: 377 T: 0 other:
Query Match	86.6%; Score 1455; DB 24; Length 1873;
Best Local Similarity	98.9%; Pred. No. 0;
Matches 1476: Conservative	0; Mismatches 15; Indels 2; Gaps 1
OY	190 GCCCGCGGGAGACCGAGAGCCCTGTGGATGGGAGACACTTACCTTTTCGAAGCTGA 249
DB	380 GCGGGAGACGAACTGAGAGGCCCTGTGGAGTGGAAGACACTTGCATTTCGAAGCTGA 439

QY	250	GATTGAGCAGAAATCAAGAGATACAAATATGCCAGATCAACAGCAACTCTTCATGAGCTT	309
Db	440	GACTGAGCAGAAATCAAGAGATACAAATATGCCAGATCAACAGCAACTCTTCATGAGCTT	499
QY	310	GAACAGAGACGGTCTTACACAGGCTTATCAAGTTACACTGAAGCTGTGTGCCCTGT	369
Db	500	GAACAGAGACGGTCTTACACAGGCTTATCAAGTTACAGTTCAAGCTGTGTGCCCTGT	559
QY	370	CTCTGTGGCCCTCCAGCAAGAGCCACCTCCCTGTGAGATGCCGGGGGGGGCCAGAGC	429
Db	560	CTCTGTGGCCCTCCAGCAAGAGCCACCTCCCTGTGAGATGCCGGGGGGGGCCAGAGC	619
QY	430	GGGCACAAGTGTACAGGGCCCGCACTCTCTTACTCGCCCAAGATGCTGTCAAGCACT	489
Db	620	GGGCACAAGTGTACAGGGCCCGCACTCTCTTACTCGCCCAAGATGCTGTCAAGCACT	679
QY	480	GCATGTGCTGTACGCACACAGGGCAGTGAAGTCAATTGAGGCCCTGTTCGAAAGTCTT	549
Db	680	ACATGTGCTGTACGCACACAGGGCAGTGAAGTCAATTGAGGCCCTGTTCGAAAGTCTT	739
QY	550	GGTGTGGATGACCCCGGCAAGTTGGACCTCTTGAAGCGGCTGAGCGCTCACGGCCAGT	609
Db	740	GGTGTGGATGACCCCGGCAAGTTGGACCTCTTGAAGCGGCTGAGCGCTCACGGCCAGT	799
QY	610	GTACTTGGCGAAGCGTGTGATGATGATGACAGCCCTGCGGGCTGCAGGCTCTGTGCAGGGCC	669
Db	800	GTACTTGGCGAAGCGTGTGATGATGATGACAGCCCTGCGGGCTGCAGGCTCTGTGCAGGGCC	859
QY	670	CAGTGACAAAGGCCCTGAGCCTTTGTCTGAAGAAATGACTCTGGGGAGGTGAACGTGGGA	729
Db	860	CAGTGACAAAGGCCCTGAGCCTTTGTCTGAAGAAATGACTCTGGGGAGGTGAACGTGGGA	919
QY	730	CGCCCTTGACAGTGGCCTGAACTACATAACTCTTACCTGCTGACAGCGGGAGAGAGAGA	789
Db	920	CGCCCTTGACAGTGGCCTGAACTACATAACTCTTACCTGCTGACAGCGGGAGAGAGAGA	979
QY	790	GCACCTCCGCGAGATCTGACAGAACTACTCTATTGCCCGCAGAAAGATCTCAAGAGGCCCT	849
Db	980	GCACCTCCGCGAGATCTGACAGAACTACTCTATTGCCCGCAGAAAGATCTCAAGAGGCCCT	1039
QY	850	GCACGCCCTGCCCTTTGGGTGACCTTGTATACCCCCAGGTGAGAGCACAGCAGGCAG	909
Db	1040	GCACGCCCTGCCCTTTGGGTGACCTTGTATACCCCCAGGTGAGAGCACAGCAGGCAG	1099
QY	910	CGCCCAAGGCGCGCGGTGAGATGACAGGGCCAGTGGGGCTGTGGAAATGAGATGTGCA	969
Db	1100	CGCCCAAGGCGCGCGGTGAGATGACAGGGCCAGTGGGGCTGTGGAAATGAGATGTGCA	1159
QY	970	TGAGAGCCCTCTGTGTGTGTGGGGGAATGAGCCAGAAACAGCAGAAATGACTGTGCCCTG	1029
Db	1160	TGAGAGCCCTCTGTGTGTGTGGGGGAATGAGCCAGAAACAGCAGAAATGACTGTGCCCTG	1219
QY	1030	TGTCCACCTATGGGTGTAGCCAGGTATGGCTGTGCACCCCTGTGCCCTCATTTACTGGGCC	1089
Db	1220	TGTCCACCTATGGGTGTAGCCAGGTATGGCTGTGCACCCCTGTGCCCTCATTTACTGGGCC	1279
QY	1090	TTAGTGGGGCAGGGGCTGGCGTGAAGAGTGGTCCAGGGGCTGAGAGGAGAGGTGTCCACAG	1149
Db	1280	TTAGTGGGGCAGGGGCTGGCGTGAAGAGTGGTCCAGGGGCTGAGAGGAGAGGTGTCCACAG	1339
QY	1150	AGAACTCTCTCAATTTTGTCTCAGAAATGAAATCTTGGAGACCTGTCAACAGAAACA	1209
Db	1340	AGAACTCTCTCAATTTTGTCTCAGAAATGAAATCTTGGAGACCTGTCAACAGAAACA	1399
QY	1210	GGGTCTATTTTGCAGGGGTGACGGCCCTCATCTATGAGGAAAGTTTGGATCTTGAATG	1269
Db	1400	GGGTCTATTTTGCAGGGGTGACGGCCCTCATCTATGAGGAAAGTTTGGATCTTGAATG	1459
QY	1270	TGGTCTAGAGATTCCTTATCAGAGACTAAAGGTGGTCTCAGAAATAGAGCAGCATATGA	1329
Db	1460	TGGTCTAGAGATTCCTTATCAGAGACTAAAGGTGGTCTCAGAAATAGAGCAGCATATGA	1519
QY	1330	GGAAAGATCTTGGTTCTCTCTACAGTCCCAACTCTCTCACACACCCTGAGTCAAGGAGT	1389

```

Db      1520  GGAAGAGTCTGTTCTCTACAGTGCACCTCTACACACCTTAGGTCAGGAGT 1579
Oy      1390  GCTGCTCAGACAGTACAGCATGTCCTTAATGCTTATATGAGAGAGATGTCCTGGGCA 1449
Db      1580  GCTGCTCAGACAGTACAGCATGTCCTTAATGCTTATATGAGAGAGATGTCCTGGGCA 1639
Oy      1450  GGGTGTGTGTATGATGGGACATGGCCAGATTCATACCTATTGCTTAATCAAGCAG 1509
Db      1640  GGGTGTGTGTATGATGGGACATGGCCAGATTCATACCTATTGCTTAATCAAGCAG 1699
Oy      1510  GGTCTCTCCCTCAGGTGTTTTTATGAGTGGGATGATGTATGTATGTGTGGTGGCTC 1569
Db      1700  GGTCTCTCCCTCAGGTGTTTTTATGAGTGGGATGATGTATGTATGTGTGGTGGCTC 1759
Oy      1570  AGCTGAATGCTCTCTGTGGGGAAGGGGTTGGGGTGACAGTCAATCAGC--CCTGGAG 1627
Db      1760  AGCTGAATGCTCTCTGTGGGGAAGGGGTTGGGGTGACAGTCAATCAGCAGGGGCTG 1819
Oy      1628  CTGAGAGAAATGGCCATTAAGATTTCAAGTCCAAAAAAGGAGAGAGAGAGAGAGAG 1680
Db      1820  CTGAGAGAAATGGCCATTAAGATTTCAAGTCCAAAAAAGGAGAGAGAGAGAGAGAG 1872

```

RESULT 6

AB555593 standard; cDNA; 1873 BP.

AB555593;

19-DEC-2002 (first entry)

Human cDNA encoding tumour suppressor RASSFL.A variant 3.

Human; ss; gene; tumour suppressor; RASSFL.A; cancer; breast cancer; SNP; single nucleotide polymorphism; DNA methylation; lung cancer; kidney cancer; ovarian cancer; head and neck cancer; melanoma; chromosome 3p21.3.

Homo sapiens.

Location/Qualifiers
39..1061

/*tag- a
/product- "RASSFL.A"

/*tag- b
/standard_name- "Single nucleotide polymorphism"

replace (808,6)

US2002098530-A1.

25-JUL-2002.

30-MAR-2001; 2001US-0821803.

30-MAR-2000; 2000US-193268P.

(CITY) CITY OF HOPE.

Pfeifer GP, Damann R;

WPI, 2002-690479/74.

P-PSDB; ABG71312.

Novel tumor suppressor gene, termed RASSFL, useful for the diagnosis of predisposition to cancer by analyzing its methylation status, heterozygosity or mutation

Claim 3; Page -; 57Pp; English.

The invention relates to an isolated tumour suppressor gene coding for

splice variant RASSFL.A, RASSFL.B or RASSFL.C protein or its complement, or a DNA molecule which hybridises under stringent conditions to them. Also included are naturally occurring mutants of RASSFL.A, detecting (M1) a methylated RASSFL gene, non-expressed RASSFL gene or an alteration in RASSFL where the methylation, non-expression or alteration is associated with cancer in a human, by analysing an RASSFL gene or an RASSFL gene expression product from a tissue or body fluid of the human; administering RASSFL agonists to treat cancer, a RASSFL non-human transgenic animal, a cell line from the transgenic animal, and screening for cancer therapeutics/drug candidates useful in treating cancer resulting from a methylated or a mutation in RASSFL. (M1) is useful for detecting methylated RASSFL gene, which is useful for determining whether a human subject has or is at risk for developing cancer. The method involves detecting the methylation or non-expression of the gene or the presence or absence of a genetic polymorphism as in the RASSFL gene of the subject, where the methylation or non-expression or the presence of the genetic polymorphism identifies a subject that has or is at risk for developing cancer. The mutants are useful for screening for drug candidates useful in treating cancer resulting from the RASSFL gene. Analysis of the RASSFL gene is useful in the diagnosis of predisposition to cancer, including lung, breast, kidney, ovarian, head and neck cancer and melanoma. The association between the RASSFL gene and cancer permits the early presymptomatic screening of individuals to identify those at risk for developing cancer. RASSFL protein is useful for identifying agonists of the biological function of an RASSFL protein. RASSFL, its encoding nucleic acids, antibodies and compounds identified by the screening assays are useful for treating cancer. The gene for RASSFL is located on chromosome 3p21.3. The present sequence encodes a natural variant of RASSFL splice variant RASSFL.A.

Note: The present sequence is not shown in the specification but was created by the indexer using the information in claim 3 and the RASSFL.A sequence appearing as AB555574.

Sequence 1873 BP; 395 A; 516 C; 584 G; 378 T; 0 other;

Query Match 86.6%; Score 1455; DB 24; Length 1873;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 1476; Conservative 0; Mismatches 15; Indels 2; Gaps 1;

```

Oy      190  GCCGCCGCCGACACGACGAGACCTGTGATGGAGAGACCTGCTTCAAGTGA 249
Db      380  GCGGACACGAAACGAGAGAGCTGTGATGGAGAGACCTGCTTCAAGTGA 439
Oy      250  GATTGAGCAGAAATCAAGAGTACCAATGCCAGATCAACAGCAACCTCTCATGAGCTT 309
Db      440  GATTGAGCAGAAATCAAGAGTACCAATGCCAGATCAACAGCAACCTCTCATGAGCTT 499
Oy      310  GAACAAGAGCGCTTCTACAGAGCTTCATCAAGTTCAGTGAAGTGGTGGCTGT 369
Db      500  GAACAAGAGCGCTTCTACAGAGCTTCATCAAGTTCAGTGAAGTGGTGGCTGT 559
Oy      370  CTCTGCTCTCCACAGCAAGACCACTCTCTCAGAGTCCCGCGGCGGCCAGAGACG 429
Db      560  CTCTGCTCTCCACAGCAAGACCACTCTCTCAGAGTCCCGCGGCGGCCAGAGACG 619
Oy      430  GGGCACAAGTGTACAGGCGCCGCACTTCTTACCTGCGCCCAAGAGTGTCAAGCACT 489
Db      620  GGGCACAAGTGTACAGGCGCCGCACTTCTTACCTGCGCCCAAGAGTGTCAAGCACT 679
Oy      490  GCATGTGCTGCACGACCAAGGGGACGATGATGAGGCGCTGCTGCAAGTCTT 549
Db      680  ACATGTGCTGCACGACCAAGGGGACGATGATGAGGCGCTGCTGCAAGTCTT 739
Oy      550  GGTGTGATGACCCCGCAGATTTGACACTTTGAGCGCGCTGAGCTCAGGCAAGT 609
Db      740  GGTGTGATGACCCCGCAGATTTGACACTTTGAGCGCGCTGAGCTCAGGCAAGT 799
Oy      610  GTACTTGGGAAGCTGTTGATGATGAGCAGCCCTCGGCTGGCGCTCTGCGAGGCGC 669
Db      800  GTACTTGGGAAGCTGTTGATGATGAGCAGCCCTCGGCTGGCGCTCTGCGAGGCGC 859
Oy      670  CAGTGAACAGGCGCTGAGCTTTGTCTGAAGGAATGACTTGGGAGGTGAACCTGGGA 729

```

```

Db      |||||||
860 CAGTGCACAAAGCCCTGAGCTTTGCTCTGTAAGAAAATGCTGTGGGAGTGAACCTAGCGGA 919
Oy      |||||||
730 CGCCTTCAGCATGCTGTAACATACATTAATCTTACGTATCTGACAGCGGAGAGAGAGA 789
Db      |||||||
920 CGCCTTCAGCATGCTGTAACATACATTAATCTTACGTATCTGACAGCGGAGAGAGAGA 979
Oy      |||||||
790 GCACCTCCGCCAGATCTGTCAGAACTACTCTATTGCCGCCAGAAAGATCAAGAGGCCCT 849
Db      |||||||
980 GCACCTCCGCCAGATCTGTCAGAACTACTCTATTGCCGCCAGAAAGATCAAGAGGCCCT 1039
Oy      |||||||
850 GCACCTCCGCCAGATCTGTCAGAACTACTCTATTGCCGCCAGAAAGATCAAGAGGCCCT 909
Db      |||||||
1040 GCACCTCCGCCAGATCTGTCAGAACTACTCTATTGCCGCCAGAAAGATCAAGAGGCCCT 1099
Oy      |||||||
910 CGCCTTCAGCATGCTGTAACATACATTAATCTTACGTATCTGACAGCGGAGAGAGAGA 969
Db      |||||||
1100 CGCCTTCAGCATGCTGTAACATACATTAATCTTACGTATCTGACAGCGGAGAGAGAGA 1159
Oy      |||||||
970 TGGAGGCCCTCTGCTGCTGGGGAAATGAGCCAGAGAACAGGAAAGTACCTTCTCTCTG 1029
Db      |||||||
1160 TGGAGGCCCTCTGCTGCTGGGGAAATGAGCCAGAGAACAGGAAAGTACCTTCTCTCTG 1219
Oy      |||||||
1030 TGTCCACCTATATGGGTGTAGCCAGATATGGCTCTGCAACCCCTCTGCTTACTTACTG 1089
Db      |||||||
1220 TGTCCACCTATATGGGTGTAGCCAGATATGGCTCTGCAACCCCTCTGCTTACTTACTG 1279
Oy      |||||||
1090 TTAGTGGGCCAGAGGCTGCTGAGAAAGCTGTCAGAGGCTGTCAGAGAGAGAGTGGTCAG 1149
Db      |||||||
1280 TTAGTGGGCCAGAGGCTGCTGAGAAAGCTGTCAGAGGCTGTCAGAGAGAGAGTGGTCAG 1339
Oy      |||||||
1150 AGAAGCTCTCTCAATTTTGTCTCAGAAAGTAAATCTTGGAGACCCCTGCAACAGACACA 1209
Db      |||||||
1340 AGAAGCTCTCTCAATTTTGTCTCAGAAAGTAAATCTTGGAGACCCCTGCAACAGACACA 1399
Oy      |||||||
1210 GGGTATGTTGACAGGGGTGAGGGCCCTATCTATGAGAGAAAGTTTGGATCTTGAATG 1269
Db      |||||||
1400 GGGTATGTTGACAGGGGTGAGGGCCCTATCTATGAGAGAAAGTTTGGATCTTGAATG 1459
Oy      |||||||
1270 TGGTCTCAGAGATATCTTATCAGAGCTAAAGGTGGTCTCAGAAATTAAGAGGATGA 1329
Db      |||||||
1460 TGGTCTCAGAGATATCTTATCAGAGCTAAAGGTGGTCTCAGAAATTAAGAGGATGA 1519
Oy      |||||||
1330 GGAAGAGCTTGTGTTTCTCTCAGAGTGCACCACTCTCAGACACCTGAGGTGAGGAGT 1389
Db      |||||||
1520 GGAAGAGCTTGTGTTTCTCTCAGAGTGCACCACTCTCAGACACCTGAGGTGAGGAGT 1579
Oy      |||||||
1390 GGTGCTCAGATATGCTTATGAGAGTGCCTTATGCTTATGAGAGAGATGCTCCCTGGCCA 1449
Db      |||||||
1580 GGTGCTCAGATATGCTTATGAGAGTGCCTTATGCTTATGAGAGAGATGCTCCCTGGCCA 1639
Oy      |||||||
1450 GGTGCTGCTGATGATGAGCAGTGGCCAGTTCATACCTTATTTGCTAATCAAGCCAG 1509
Db      |||||||
1640 GGTGCTGCTGATGATGAGCAGTGGCCAGTTCATACCTTATTTGCTAATCAAGCCAG 1699
Oy      |||||||
1510 GGTGCTGCTGATGATGAGCAGTGGCCAGTTCATACCTTATTTGCTAATCAAGCCAG 1569
Db      |||||||
1700 GGTGCTGCTGATGATGAGCAGTGGCCAGTTCATACCTTATTTGCTAATCAAGCCAG 1759
Oy      |||||||
1570 AGCTGAATGCTGCTGATGAGCAGTGGCCAGTTCATACCTTATTTGCTAATCAAGCCAG 1627
Db      |||||||
1760 AGCTGAATGCTGCTGATGAGCAGTGGCCAGTTCATACCTTATTTGCTAATCAAGCCAG 1819
Oy      |||||||
1628 CTGAGAGAAATGGCTCAATTAAGATTTCAAGATCCAAAAAAGAGAGAGAGAGAGAGAG 1680
Db      |||||||
1820 CTGAGAGAAATGGCTCAATTAAGATTTCAAGATCCAAAAAAGAGAGAGAGAGAGAGAG 1872

```

RESULT 7
 ABS55594
 ID ABS55594 standard; cDNA; 1873 BP.
 XX
 AC ABS55594;

```

XX 19-DEC-2002 (first entry)
DT Human cDNA encoding tumour suppressor RASSF1.A variant 4.
XX
DE Human: ss; gene; tumour suppressor; RASSF1.A; cancer; breast cancer;
XX SNP; single nucleotide polymorphism; DNA methylation; lung cancer;
XX kidney cancer; ovarian cancer; head and neck cancer; melanoma;
XX chromosome 3p21.3.
OS Homo sapiens.
EH
FH
FT CDS
FT /tag= a
FT /product= "RASSF1.A"
FT variation
FT /tag= b
FT /standard_name= "Single nucleotide polymorphism"
FT replace (1044,g)
FT /tag= c
PN US2002098530-A1.
XX 25-JUL-2002.
PD
XX 30-MAR-2001; 2001US-0821803.
XX 30-MAR-2000; 2000US-193268P.
PR (CITY ) CITY OF HOPE.
PA
XX Pfeiffer GP, Dammann R;
XX MPI: 2002-690479/74.
XX P-PSDB; ABG71313.
DR
XX Novel tumor suppressor gene, termed RASSF1, useful for the diagnosis of
PT predisposition to cancer by analyzing its methylation status,
PT heterozygosity or mutation
XX
XX Claim 3; Page -: 57pp; English.
XX
XX The invention relates to an isolated tumour suppressor gene coding for
XX splice variant RASSF1.A, RASSF1.B or RASSF1.C protein or its complement,
XX or a DNA molecule which hybridises under stringent conditions to them.
XX Also included are naturally occurring mutants of RASSF1.A, detecting (M1)
XX a methylated RASSF1 gene, non-expressed RASSF1 gene or an alteration in
XX RASSF1 where the methylation, non-expression or alteration is associated
XX with cancer in a human, by analysing an RASSF1 gene or an RASSF gene
XX expression product from a tissue or body fluid of the human;
XX administering RASSF1 agonists to treat cancer, a RASSF1 non-human
XX transgenic animal, a cell line from the transgenic animal, and
XX screening for cancer therapeutics/drug candidates useful in treating
XX cancer resulting from a methylated or a mutation in RASSF1.
XX (M1) is useful for detecting methylated RASSF1 gene, which is
XX useful for determining whether a human subject has or is at risk for
XX developing cancer. The method involves detecting the methylation or
XX non-expression of the gene or the presence or absence of a genetic
XX polymorphism as in the RASSF1 gene of the subject, where the
XX methylation or non-expression or the presence of the genetic
XX polymorphism identifies a subject that has or is at risk for developing
XX cancer. The mutants are useful for screening for drug candidates useful
XX in treating cancer resulting from the RASSF1 gene. Analysis of the RASSF1
XX gene is useful in the diagnosis of predisposition to cancer, including
XX lung, breast, kidney, ovarian, head and neck cancer and melanoma. The
XX association between the RASSF1 gene and cancer permits the early
XX presymptomatic screening of individuals to identify those at risk for
XX developing cancer. RASSF1 protein is useful for identifying agonists of
XX the biological function of an RASSF1 protein. RASSF1, its encoding
XX nucleic acids, antibodies and compounds identified by the screening
XX assays are useful for treating cancer. The gene for RASSF1 is located
XX on chromosome 3p21.3. The present sequence encodes a natural variant of

```

CC RASFL1 splice variant RASFL1.A.
 CC Note: The present sequence is not shown in the specification but
 CC was created by the indexer using the information in claim 3 and the
 CC RASFL1.A sequence appearing as AB555574.
 XX
 XX
 S0 Sequence 1873 BP: 395 A; 516 C; 584 G; 378 T; 0 other:

Query Match 86.6%; Score 1455; DB 24; Length 1873;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 1476; Conservative 0; Mismatches 15; Indels 2; Gaps 1;

OY 190 GCCCGCGCGGACGAGCCGCTGAGTGGAGACACCTTCTCAAGCTGA 249
 DB 380 GCGGAGACGAGAGCTGAGCCCTGTGAGTGGAGACACCTTCTCAAGCTGA 439
 OY 250 GATTGAGCAGAGATCAAGAGTACAAATGCCAGATCAACAACTCTTCATGAGCTT 309
 DB 440 GATTGAGCAGAGATCAAGAGTACAAATGCCAGATCAACAACTCTTCATGAGCTT 499
 OY 310 GAACAAGAGCGGTTCTTACACAGGCTTCATCAAGGTTCAAGTGAAGCTGTGCGCCCTGT 369
 DB 500 GAACAAGAGCGGTTCTTACACAGGCTTCATCAAGGTTCAAGTGAAGCTGTGCGCCCTGT 559
 OY 370 CTCTGTGCGCTCCGACGAAGCCACCTCTTGAAGATGCCGGGGGGGCCGACGAG 429
 DB 560 CTCTGTGCGCTCCGACGAAGCCACCTCTTGAAGATGCCGGGGGGGCCGACGAG 619
 OY 430 GGGCACAAGTGTACAGGCGCCGACTCTTCTTACCTGCGCAAGATGCTGTCAAGCAGCT 489
 DB 620 GGGCACAAGTGTACAGGCGCCGACTCTTCTTACCTGCGCAAGATGCTGTCAAGCAGCT 679
 OY 490 GCATGTGCTGTACAGCAGCAGAGGAGCGATGATGAGGCGCTGCTGCAAAAGTCTT 549
 DB 680 ACATGTGCTGTACAGCAGCAGAGGAGCGATGATGAGGCGCTGCTGCAAAAGTCTT 739
 OY 550 GGTGTGATGATACCCCGCAAGTGTGACCTTGTGAGGCGCTGAGGCGTCAAGGCAAGT 609
 DB 740 GGTGTGATGATACCCCGCAAGTGTGACCTTGTGAGGCGCTGAGGCGTCAAGGCAAGT 799
 OY 610 GTACTTGCAGAGCTGTTGATGATGAGCAGCCCTGCGGCTGCGGCTCTGCGAGGCGC 669
 DB 800 GTACTTGCAGAGCTGTTGATGATGAGCAGCCCTGCGGCTGCGGCTCTGCGAGGCGC 859
 OY 670 CAGTGAAGAAGGCGCTGAGCTTGTCTGAGAGAAATGACTCTGGGAGAGTGAAGTGGGA 729
 DB 860 CAGTGAAGAAGGCGCTGAGCTTGTCTGAGAGAAATGACTCTGGGAGAGTGAAGTGGGA 919
 OY 730 CGCCTTACAGTGTGCTGAACTAATCTTCTACGTATCTGAGGCGGAGAGAGAGA 789
 DB 920 CGCCTTACAGTGTGCTGAACTAATCTTCTACGTATCTGAGGCGGAGAGAGAGA 979
 OY 790 GCACCTCCGCGAGTCTGAGAGTACTCTATTTGCGCGCAGAGATCCAAAGGCGCT 849
 DB 980 GCACCTCCGCGAGTCTGAGAGTACTCTATTTGCGCGCAGAGATCCAAAGGCGCT 1039
 OY 850 GCAGGCGCTGCGGCTTGGGAGTACTCTTGTACCCCGCAGTGGAGAGAGAGAGAGAG 909
 DB 1040 GCAGGCGCTGCGGCTTGGGAGTACTCTTGTACCCCGCAGTGGAGAGAGAGAGAGAG 1099
 OY 910 CGCCAAAGTGGGCTGCTGTGAGTGTGACAGGCGCAGTGGGCGCTGTGGAATGATGTGCA 969
 DB 1100 CGCCAAAGTGGGCTGCTGTGAGTGTGACAGGCGCAGTGGGCGCTGTGGAATGATGTGCA 1159
 OY 970 TGGAGGCGCTGCTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1029
 DB 1160 TGGAGGCGCTGCTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1219
 OY 1030 TGTCCACCTAAGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1089
 DB 1220 TGTCCACCTAAGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1279
 OY 1090 TTAGTGGCGAGGCTGCGCTGAGAGAGTGTCTGAGGCGTGCAGAGAGAGAGAGAGAG 1149

DB 1280 TTAGTGGCGAGGCTGCGCTGAGAGAGTGTCTGAGAGAGAGAGAGAGAGAGAGAGAG 1339
 OY 1150 AGAAGTCTCTCAATTTTGTCTCAGAGTGAATAATCTTGGAGAGAGAGAGAGAGAGAGAG 1209
 DB 1340 AGAAGTCTCTCAATTTTGTCTCAGAGTGAATAATCTTGGAGAGAGAGAGAGAGAGAG 1399
 OY 1210 GGGTCATGTTTGGAGAGGCTGAGGCGCTCATCTATGAGAGAGAGAGAGAGAGAGAGAG 1269
 DB 1400 GGGTCATGTTTGGAGAGGCTGAGGCGCTCATCTATGAGAGAGAGAGAGAGAGAGAGAG 1459
 OY 1270 TGGTCTCAGATATCTTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1329
 DB 1460 TGGTCTCAGATATCTTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1519
 OY 1330 GGAAGAGCTTGTGTTTCTCTACAGTGCACAACTCTCAGAGAGAGAGAGAGAGAGAGAG 1389
 DB 1520 GGAAGAGCTTGTGTTTCTCTACAGTGCACAACTCTCAGAGAGAGAGAGAGAGAGAGAG 1579
 OY 1390 GCTGGCTCAGATACAGCATGTGCTTAATGCTTATATGAGAGAGAGAGAGAGAGAGAG 1449
 DB 1580 GCTGGCTCAGATACAGCATGTGCTTAATGCTTATATGAGAGAGAGAGAGAGAGAGAG 1639
 OY 1450 GGGTCTGTAATGTGGGAG 1509
 DB 1640 GGGTCTGTAATGTGGGAG 1699
 OY 1510 GGTCTCTCCCTCAGAGTGTGTTTATGAGAGTGCAGTGAATGTGATGATGTGGGCGCT 1569
 DB 1700 GGTCTCTCCCTCAGAGTGTGTTTATGAGAGTGCAGTGAATGTGATGATGTGGGCGCT 1759
 OY 1570 AGCTGAATGCTCTCTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1627
 DB 1760 AGCTGAATGCTCTCTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1819
 OY 1628 CTGAGAGAAATGGCTCAATAAAGATTCAAGATCCAAAAAAGAGAGAGAGAGAGAGAG 1680
 DB 1820 CTGAGAGAAATGGCTCAATAAAGATTCAAGATCCAAAAAAGAGAGAGAGAGAGAGAG 1872

RESULT 8
 ABS55575
 ID ABS55575 standard; cDNA: 1664 BP.
 AC ABS55575;
 DT 19-DEC-2002 (first entry)
 XX
 DE Human cDNA encoding tumour suppressor RASFL1.B.
 XX
 KW Human; ss; gene; tumour suppressor; RASFL1.B; cancer; breast cancer;
 KW DNA methylation; lung cancer; kidney cancer; ovarian cancer;
 KW head and neck cancer; melanoma; chromosome 3p21.3.
 XX
 OS Homo sapiens.
 XX
 FH key Location/Qualifiers
 FT CDS 282..851
 FT /tag= a
 FT /product= "RASFL1.B"
 XX
 PD 25-JUL-2002.
 XX
 PF 30-MAR-2001; 2001US-0821803.
 XX
 PR 30-MAR-2000; 2000US-193268P.
 XX
 PA (CITY) CITY OF HOPE.
 XX
 PI Pfelfer GP, Dammann R;
 XX
 DR WPI: 2002-690479/74.

DR P-PSDB: ABG71308.
XX Novel tumor suppressor gene, termed RASSF1, useful for the diagnosis of
PT predisposition to cancer by analyzing its methylation status,
PT heterozygosity or mutation
XX
XX Claim 2; Page 30-32; 57pp; English.
XX
XX The invention relates to an isolated tumour suppressor gene coding for
CC splice variant RASSF1.A, RASSF1.B or RASSF1.C protein or its complement,
CC or a DNA molecule which hybridizes under stringent conditions to them.
CC Also included are naturally occurring mutants of RASSF1.A, detecting (M1)
CC a methylated RASSF1 gene, non-expressed RASSF1 gene or an alteration in
CC RASSF1 where the methylation, non-expression or alteration is associated
CC with cancer in a human, by analysing a RASSF1 gene or an RASSF gene
CC expression product from a tissue or body fluid of the human;
CC administering RASSF1 agonists to treat cancer, a RASSF1 non-human
CC transgenic animal, a cell line from the transgenic animal, and
CC screening for cancer therapeutics/drug candidates useful in treating
CC cancer resulting from a methylated or a mutation in RASSF1.
CC (M1) is useful for detecting methylated RASSF1 gene, which is
CC useful for determining whether a human subject has or is at risk for
CC developing cancer. The method involves detecting the methylation or
CC non-expression of the gene or the presence or absence of a genetic
CC polymorphism as in the RASSF1 gene of the subject, where the
CC methylation or non-expression or the presence of the genetic
CC polymorphism identifies a subject that has or is at risk for developing
CC cancer. The mutants are useful for screening for drug candidates useful
CC in treating cancer resulting from the RASSF1 gene. Analysis of the RASSF1
CC gene is useful in the diagnosis of predisposition to cancer, including
CC lung, breast, kidney, ovarian, head and neck cancer and melanoma. The
CC association between the RASSF1 gene and cancer permits the early
CC presymptomatic screening of individuals to identify those at risk for
CC developing cancer. RASSF1 protein is useful for identifying agonists of
CC the biological function of an RASSF1 protein. RASSF1, its encoding
CC nucleic acids, antibodies and compounds identified by the screening
CC assays are useful for treating cancer. The gene for RASSF1 is located
CC on chromosome 3p21.3. The present sequence encodes the RASSF1 splice
CC variant RASSF1.B.
XX
SQ Sequence 1664 BP; 359 A; 436 C; 506 G; 363 T; 0 other;
Query Match 86.0%; Score 1445.6; DB 24; Length 1664;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1477; Conservative 0; Mismatches 14; Indels 3; Gaps 2;
QY 190 GCCGCGCCGGGACAGAGAGCGCTGTGAGTGGGAGACACCTGACCTTCTCAAGCTGA 249
DB 170 GCGGGACAGCAAGCTGTGAGCTGTGAGTGGGAGACACCTGACCTTCTCAAGCTGA 229
QY 250 GATTGAGCAGAAAGTCAAGAGTCAATGAGTCAAGTCAAGCAAGCAAGCTTCTCAAGCTT 309
DB 230 GATTGAGCAGAAAGTCAAGAGTCAATGAGTCAAGTCAAGCAAGCAAGCTTCTCAAGCTT 289
QY 310 GAAACAAGAGCGTTCTTACACAGCGTTTCAATCAAGTTCAAGCTGAGTGGCCCTGT 369
DB 290 GAACAAGAGCGTTCTTACACAGCGTTTCAATCAAGTTCAAGCTGAGTGGCCCTGT 349
QY 370 CTCTGAGCCCTCAGAGAAAGCACCCTCTTGAAGAGTGGCCGGGGGGCCCAAGAGC 429
DB 350 CTCTGAGCCCTCAGAGAAAGCACCCTCTTGAAGAGTGGCCGGGGGGGGCCCAAGAGC 409
QY 430 GGGCACAAGTGTACAGCGCGCGCACTTCTTTTACTGTGCCAAGAGTGTCTCAAGACCT 489
DB 410 GGGCACAAGTGTACAGCGCGCGCACTTCTTTTACTGTGCCAAGAGTGTCTCAAGACCT 469
QY 490 GCATGTGCTGTCAAGCAAGGGCAGTGAATGATTTAGAGCCCTGCTGCGAAAGTTCTT 549
DB 470 GCATGTGCTGTCAAGCAAGGGCAGTGAATGATTTAGAGCCCTGCTGCGAAAGTTCTT 529
QY 550 GGTGGTGAATGAGCCCGCAAGTTTGCACCTTTGAGCGCGTGAAGCTCAAGCCCAAGT 609
DB 530 GGTGGTGAATGAGCCCGCAAGTTTGCACCTTTGAGCGCGTGAAGCTCAAGCCCAAGT 589

QY 610 GTACTTGCAGAACTTTGGATGATGACAGCCCTGCGGCTGCGCTCTCTGACAGGCC 669
DB 590 GTACTTGCAGAACTTTGGATGATGATGACAGCCCTGCGGCTGCGCTCTCTGACAGGCC 649
QY 670 CAGTGAACAAGCCCTGAGCTTTTCTCTGAAGAAATGACTTGGGAGGTGAATCGGA 729
DB 650 CAGTGAACAAGCCCTGAGCTTTTCTCTGAAGAAATGACTTGGGAGGTGAATCGGA 709
QY 730 CGCCTTACAGATCCGAACTACATTAATCTTCACTATCTCAGCTACGCGGAGGAGAGGA 789
DB 710 CGCCTTACAGATCCGTAATACATTAATCTTCACTATCTCAGCTACGCGGAGGAGAGGA 769
QY 790 GCACCTCCGCAAGATCTGACAGAAAGTACTCTTATCTCCGCAAGAAATCCAAAGGCCCT 849
DB 770 GCACCTCCGCAAGATCTGACAGAAAGTACTCTTATCTCCGCAAGAAATCCAAAGGCCCT 829
QY 850 GCACGCTGCCCCCTTGGGTGACCTCTTGAACCCAGGTGGAAGCCAGACAGGACG 909
DB 830 GCACGCTGCCCCCTTGGGTGACCTCTTGAACCCAGGTGGAAGCCAGACAGGACG 889
QY 910 CGCAGAGTGGTGGGTGAGTGAAGTGAAGGCGGAGTGGGCTGTGAATGATGTGCA 969
DB 890 CGCAGAGTGGTGGGTGAGTGAAGTGAAGGCGGAGTGGGCTGTGAATGATGTGCA 949
QY 970 TGGAGGCCCTCTCTGTGCTGGGGGAATGAGCCAGAGAAAGCAAGTACCTTCTCCTG 1029
DB 950 TGGAGGCCCTCTCTGTGCTGGGGGAATGAGCCAGAGAAAGCAAGTACCTTCTCCTG 1009
QY 1030 TGTCCACTATGAGGTGATGACCAAGTATGCTGTGACACCTCTGCTCTCAATTAAGTGGCC 1089
DB 1010 TGTCCACTATGAGGTGATGACCAAGTATGCTGTGACACCTCTGCTCTCAATTAAGTGGCC 1069
QY 1090 TTATGAGGCGGAGGCGTCCCTGAGAAAGCTCTCAGAGCCGCGAGAGGAGTGTGAGAC 1149
DB 1070 TTATGAGGCGGAGGCGTCCCTGAGAAAGCTCTCAGAGCCGCGAGAGGAGTGTGAGAC 1129
QY 1150 AGAAGTCTCTCAATTTTGTCTCAGAAAGTAAATCTTGGAGACCTGCAACAGAACCA 1209
DB 1130 AGAAGTCTCTCAATTTTGTCTCAGAAAGTAAATCTTGGAGACCTGCAACAGAACCA 1189
QY 1210 GGTGATGTTTTCAGAGGGGTAGCGCCCTCAATCATGAGAAAGTTTGGATTTGAATG 1269
DB 1190 GGTGATGTTTTCAGAGGGGTAGCGCCCTCAATCATGAGAAAGTTTGGATTTGAATG 1249
QY 1270 TGTGTCAGGATATCTTATCAGAGCTAAAGGTTGGGTCTCAATTAAGCAGGCAATTGA 1329
DB 1250 TGTGTCAGGATATCTTATCAGAGCTAAAGGTTGGGTCTCAATTAAGCAGGCAATTGA 1309
QY 1330 GGAAGAGTCTGTTTCTCTCTACAGTCCCACTCTCACACACCTGAGAGTCAAGGAGT 1389
DB 1310 GGAAGAGTCTGTTTCTCTCTACAGTCCCACTCTCACACACCTGAGAGTCAAGGAGT 1369
QY 1390 GCTGCTCAGATGACAGCATGTGCTTAATGCTTCATATGAGAGAGATGCTCCTGGGCA 1449
DB 1370 GCTGCTCAGATGACAGCATGTGCTTAATGCTTCATATGAGAGAGATGCTCCTGGGCA 1429
QY 1450 GGGTGTGTGAATGAGGCGACGTGGCCAGTTCATACCTTATTTGTAATCAAGCGAG 1509
DB 1430 GGGTGTGTGAATGAGGCGACGTGGCCAGTTCATACCTTATTTGTAATCAAGCGAG 1489
QY 1510 GGTCTCTCCCTCAGGTG -TTTTTATGAAGTGCCTGAATGATTAATGATGATGCTG 1568
DB 1490 GGTCTCTCCCTCAGGTGTTTTTATGAAGTGCCTGAATGATTAATGATGATGCTG 1549
QY 1569 CAGCTGAATCCCTCTGTGTGGGAAAGGGTGGGGGTGACAGTCAATCAACG -CCTGGG 1626
DB 1550 CAGCTGAATCCCTCTGTGTGGGAAAGGGTGGGGGTGACAGTCAATCAACG -CCTGGG 1609
QY 1627 GCTGAGGAATGGCTCAATTAAGATTTCAAGATTCCTCAAGATTCCTCAAGATTCCTCA 1680
DB 1610 CTTGAGGAATGGCTCAATTAAGATTCCTCAAGATTCCTCAAGATTCCTCAAGATTCCTCA 1663

PD 16-DEC-1999.
 XX
 XX 09-JUN-1999; 99WO-IB01062.
 XX
 XX 10-JUN-1998; 98US-0088801.
 XX
 XX (FARB) BAYER CORP.
 XX
 XX Endege WO, Steilmann KE, Astle JH, Burgess CC, Bushnell SE;
 XX Carroll E, Catino TJ, Dertl A, Ford DM, Lewis ME, Monahan JE;
 XX Schlegel R;
 XX WPI; 2000-087220/07.
 XX
 XX Novel nucleic acids, used to develop products for the diagnosis and
 XX treatment of disorders involving unwanted cell proliferation,
 XX particularly cancers, especially colon cancer
 XX
 XX Claim 15; Page 383; 469pp; English.
 XX
 XX AA279917 to AA280766 represent double stranded cDNA clones isolated from
 XX the human colorectal adenocarcinoma (colon cancer) cell line SW480. The
 XX cDNA clones can be used to generate antisense oligonucleotides which
 XX can be used for antisense therapy. Methods and products from the present
 XX invention can be used for identifying and/or classifying cancerous cells
 XX present in a human tumour, particularly in solid tumours, e.g.
 XX carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones
 XX can be used for developing agents for the diagnosis and treatment of
 XX disorders involving unwanted cell proliferation, such as neoplasia,
 XX dysplasia or hyperplasia.
 XX
 XX Sequence 640 BP; 150 A; 151 C; 171 G; 150 T; 18 other;
 XX
 XX Query Match 24.7%; Score 415.2; DB 21; Length 640;
 XX Best Local Similarity 94.8%; Pred. No. 1.4e-95;
 XX Matches 437; Conservative 0; Mismatches 23; Indels 1; Gaps 1;
 XX
 XX 941 GCCAGTGGGCGCTGTGGAATGAGTGTGATGAGGCGCTCTGTGGGGGAATGAGCC 1000
 XX 13 GCCAGTGGGCGCTGTGGAATGAGTGTGATGAGGCGCTCTGTGGGGGAATGAGCC 72
 XX
 XX 1001 CAGAGAACGCGAAGAGTGTGCTCCCTGTGTCACCTATGAGGTGAGCCAGGTATGCT 1060
 XX 73 CAGAGAACGCGAAGAGTGTGCTCCCTGTGTCACCTATGAGGTGAGCCAGGTATGCT 132
 XX
 XX 1061 CTGACACCCCTCTGCCCTCAATTAAGTGTGAGGCGCTTGTGAGGCGCTCCCTGAGAACTGC 1120
 XX 133 CTGACACCCCTCTGCCCTCAATTAAGTGTGAGGCGCTTGTGAGGCGCTCCCTGAGAACTGC 192
 XX
 XX 1121 TCCAGGCGCTGACAGAGAGTGTGACAGAGAACTCTCTCAATTTTGTCTCAGAAATG 1180
 XX 193 TCCAGGCGCTGACAGAGAGTGTGACAGAGAACTCTCTCAATTTTGTCTCAGAAATG 252
 XX
 XX 1181 AAAATCTTGGAGACCTCGAACAACAGAGGCTCATGTTTGGCAGGGGTACGGCCCTCAT 1240
 XX 253 AAAATCTTGGAGAACTCGAACAACAGAGGCTCATGTTTGGCAGGGGTACGGCCCTCAT 312
 XX
 XX 1241 CTATGAGGAAGATTGATCTTGAATGTGTCTCAGAAATCTTATCAGAGCTAAG 1300
 XX 313 CTATGAGGAAGATTGATCTTGAATGTGTCTCAGAAATCTTATCAGAGCTAAG 372
 XX
 XX 1301 GTGGGTGCTCAGAAATTAAGCAGGCA-TTGAGGAAGAGTCTTGGTTTCTCTCACTGCG 1359
 XX 373 GTGGGTGCTCAGAAATTAAGCAGGCAATTTGANGAAAAATCTTGGGTCTCTTTACATGCG 432
 XX
 XX 1360 AACTCTCTCAGACACCTGAGGTGAGGAGTGTGCTGCTACA 1400
 XX 433 CACTTCTTACACACCTTGTGAGGCAAGAAATGCTTCTTACA 473
 XX
 XX RESULT 11
 XX AAS38571
 XX ID AAS38571 standard; cDNA; 381 BP.

XX
 XX AAS38571;
 XX
 XX AC 17-DEC-2001 (first entry)
 XX
 XX DT Novel human diagnostic and therapeutic gene #1629.
 XX
 XX DE Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic; ss.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200166753-A2.
 XX
 XX PD 13-SEP-2001.
 XX
 XX PF 09-MAR-2001; 2001WO-US07787.
 XX
 XX PR 09-MAR-2000; 2000US-0188609.
 XX
 XX PA (CHIR) CHIRON CORP.
 XX PA (HYSE-) HYSEQ INC.
 XX
 XX PI Williams LT, Escobedo J, Inula MA, Garcia PD, Sudduth-Klinger J;
 XX Reinhard C, Randazzo F, Kennedy GC, Pot D, Kassam A, Lamson G;
 XX Drmanac R, Crivenjakov R, Dickson M, Drmanac S, Labat I;
 XX Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
 XX
 XX DR WPI; 2001-530177/58.
 XX
 XX New polynucleotides and polypeptides, useful for diagnosis and
 XX treatment of breast, lung and colon cancer -
 XX
 XX Claim 1; Page 1004; 1193pp; English.
 XX
 XX The invention relates to new polynucleotides and polypeptides, useful for
 XX diagnosis and treatment of breast, lung and colon cancer. The sequences
 XX can be used in detecting differentially expressed genes correlated with a
 XX cancerous state of a mammalian cell, comprising detecting at least one
 XX differentially expressed gene product in a test sample derived from a
 XX cell suspected of being cancerous. They can also be used to inhibit
 XX tumour growth by modulating expression of a gene product. AAS36943-
 XX AAS33338 represent novel human diagnostic and therapeutic coding
 XX sequences of the invention.
 XX
 XX Sequence 381 BP; 73 A; 103 C; 124 G; 81 T; 0 other;
 XX
 XX Query Match 22.0%; Score 368.8; DB 22; Length 381;
 XX Best Local Similarity 99.5%; Pred. No. 7.4e-84;
 XX Matches 370; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 848 CTGACAGCCCTGCCCCCTGGGTGACCTCTGTACCCCAAGGTGGAAGCAGACAGAGC 907
 XX 10 CGGACAGCCCTGCCCCCTGGGTGACCTCTGTACCCCAAGGTGGAAGCAGACAGAGC 69
 XX
 XX 908 AGCGCAAGTGCCTGCTGTGAGTGTGACAGGGCCAGTGGGCTGTGGAATGAGTGTG 967
 XX 70 AGCGCAAGTGCCTGCTGTGAGTGTGACAGGGCCAGTGGGCTGTGGAATGAGTGTG 129
 XX
 XX 968 CATGAGAGCCCTCTGTGCTGGGGGAATGAGCCCAAGAAACAGCAAGTACTGCTCC 1027
 XX 130 CATGAGAGCCCTCTGTGCTGGGGGAATGAGCCCAAGAAACAGCAAGTACTGCTCC 189
 XX
 XX 1028 TGTGTACACTATGAGGTGAGCAGGATGAGGCTGACCCCTGCTCCCTCATTAAGTGG 1087
 XX 190 TGTGTACACTATGAGGTGAGCAGGATGAGGCTGACCCCTGCTCCCTCATTAAGTGG 249
 XX
 XX 1088 CCTTACTGGGCCAGGGCTGCTGAGAAAGTGTCTCCAGGCTTGCACAGAGTGTGCAG 1147
 XX 250 CCTTACTGGGCCAGGGCTGCTGAGAAAGTGTCTCCAGGCTTGCACAGAGTGTGCAG 309
 XX
 XX 1148 ACAGAAATCTCTCAATTTTGTCTCAGAAAGTAAAAATCTTGGAGACCTGCAACAGAA 1207
 XX 310 ACAGAAATCTCTCAATTTTGTCTCAGAAAGTAAAAATCTTGGAGACCTGCAACAGAA 369

OY 1208 CAGGTCATGTT 1219
 DB 370 CAGGTCATGTT 381

RESULT 12
 ABX42018
 ID ABX42018 standard; cDNA: 421 BP.
 AC ABX42018;
 XX 20-FEB-2003 (first entry)
 DT
 XX Bovine EST associated with lactation/muscle/fat deposition #7183.
 DE
 XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KM gene analysis; cattle breeding.
 XX
 OS Bos Taurus.
 XX
 PN US2002137139-A1.
 XX
 PD 26-SEP-2002.
 XX
 PF 24-SEP-2001; 2001US-0960352.
 XX
 PR 12-JAN-1999; 99US-115707P.
 PR 11-JAN-2000; 2000US-0480902.
 XX
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX
 PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 DR WPI; 2003-110599/10.
 XX
 PT New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and
 PT analysis, cattle breeding, or for genetically improving cattle
 XX
 PS Claim 2; SEQ ID No 7183; 245bp; English.

The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are: (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non-transcribed sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid is predictive of the level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine LMFD EST (expressed sequence tag) nucleic acids.

Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: seqdata.uspto.gov/sequence.html?docid=20020137139.

XX SQ Sequence 421 BP; 86 A; 121 C; 146 G; 68 T; 0 other;
 Query Match 14.3%; Score 240.2; DB 25; Length 421;
 Best Local Similarity 86.6%; Pred. No. 4.1e-51;
 Matches 290; Conservative 0; Mismatches 36; Indels 7; Gaps 2;

OY 3 GGGGCGGTGTTGGCGCTACGAGCGCGCAGA-CTGGGGAGCGGCGGCTACGGCTATG 61
 DB |||||
 DB 87 GGGGCGGTGTTGGCGCTACGAGCGCGCAGA-CTGGGGAGCGGCGGCTACGGCTATG 146
 OY 62 GCGGAGCGGAGG-----CGCTTCTTTCGAAATGACCTGGAGCAGCAGCAGCACT 115
 DB |||||
 DB 147 GGTAGGGGAGCGGAGGAGCGCTTCTTCAGATGACTTGAACAGCAGCAGCAAGCACT 206
 OY 116 GGTACTACGACCAAGAGACTCGGAGCTCGAGCTCGAGCTCGAGTACTGCGGTAC 175
 DB |||||
 DB 207 GGTACTACGACCAAGAGACTCGGAGCTCGAGCTCGAGTACTGCGGTAC 266
 OY 176 TCGCTAGCTCGCAGGCGCGCGGAGCAGGAGCAGCAGCTGTGAGTGGAGACACCTGAC 235
 DB |||||
 DB 267 TCGCTAGCTCGCAGGCGCGCGGAGCAGGAGCAGCAGCTGTGAGTGGAGACACCTGAC 326
 OY 236 CTTTCTCAAGCTGAGATGAGCAGAGATCAAGAGATCAATGCCCAATCAACAGCAAC 295
 DB |||||
 DB 327 CTTTCTCAAGCTGAGATGAGCAGAGATCAAGAGATCAATGCCCAATCAACAGCAAC 386
 OY 296 CTTTCAATGAGCTTGAACAGGAGGCTTCTTCAAC 330
 DB |||||
 DB 387 TTGTTCAATGAGCTTGAACAGGAGGCTTCTTCAAC 421

RESULT 13
 AAA27132
 ID AAA27132 standard; cDNA: 3144 BP.
 XX
 AC AAA27132;
 XX
 DT 11-SEP-2000 (first entry)
 XX
 DE Human inflammation associated cDNA #8.
 XX
 KW Inflammation; rheumatoid arthritis; Crohn's disease; asthma;
 KW multiple sclerosis; allergy; AIDS; diabetes mellitus;
 KW antiinflammatory; gene therapy; human; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 42..839
 FT CDS /product="inflammation associated protein #8"
 XX
 PN W0200029574-A2.
 XX
 PD 25-MAY-2000.
 XX
 PF 04-NOV-1999; 99WO-US26234.
 XX
 PR 18-NOV-1998; 98US-0195292.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Walker MG, Volkmuth W, Klingler TM;
 DR WPI: 2000-387787/33.
 DR P-PSDB: AAY94451.
 XX
 PT New human inflammation-associated polypeptide useful for diagnosis,
 PT prevention and treatment of inflammatory diseases comprises product of
 PT gene coexpressed with e.g. CD16, L-selectin and IP-30 -
 XX
 PS Claim 2; Page 35-36; 43bp; English.


```

OY 270 AGTACATGGCCCATCATCAACGCAACCTCTTCATGAGCTTGACAAAGGAGCGTCTTACA 329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 232 GCTACAACAGCGCGAGAGAAAGTGCCTGGGCAATGAACCTGAAGACGGCACCTACA 291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 330 CAGGCTTCATCAAGAGTTCAAGCTGAGTGGCGCCCTGTCTGTGTGCCCCCTCAGCAAGA 389
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 292 CGGTTTCATCAAAAGTGCATCTGAAACTCCGGCGGCTGTGACCGTGTGCTGGATCC 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 390 AGCCACCTCCTCTGACAGATGCCGGCGGGGCCAGAGACGGGGCACAAGTGTACGGCGCC 449
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 352 GGGCCCGATCCATCTATGATGCCATCAAGAGGTGAACCTGGCGGCTACACAGGACAAGC 411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 450 GCACCTCTTTACCTGCCCCAAGATGCTGTCAAGACACCTGACATGTGCTGCACAGCAAA 509
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 412 GGACATCTCTTACCTGCCCCCTAGATGCATCAAGACGCTGCACATAGACACACCA 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 510 GGGCAGCTGAAGTATGAGCCCTGCTGCGAAGTTCTTGTGTGTGATGACCCCGCA 569
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 472 CCGTCATGAGGTATCCAGGGGCTGCTCAAGAAATTCATGTGTGTGACAAATCCCA 531
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 570 AGTTGCACTCTTTGAGCGCGCTGACGCTCACGGCAAGTGTACTTCCGGAAGCTGTGG 629
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 532 AGTTGCACTCTTTTAAACGGATACACAAGGACGACAAAGTGTCTTCAGAAATCTTCA 591
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 630 ATGATGAGCAAGCCCTGCGGCTGCGGCTCCGAGAGGGCCCAAGTACAGAGCCCTGACT 689
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 592 TTGCTGACCGCCCTTACTGCGCTGCTTGTGGGCTGACACGAGAGGTCTCTCACT 651
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 690 TTGCTGAGAGAAATGACTGTGGGAGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 749
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 652 TTGCTGAGAGAAATGAACTGAGAGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 711
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 750 TACATTAATCTCTCTGATCTGTCGAGCGGAGAGAGAGACACCTCCGCAATCTTGC 809
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 712 TTCGAACTTCTCTTAACATCTGTGAAAAAGAGAGACAAATCAACAACTGCAAA 771
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 810 AGAAGTACTCTATTTGCGCGCAGAAATCCAAAGAGGCGCT 849
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 772 AGAAGTATGACAACTTAAAGCAGAACTGGAGAGGCGCTT 811
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 15

ABK93006
ID ABK93006 standard; cDNA: 303 BP.

ABK93006;

22-AUG-2002 (first entry)

DE cDNA encoding human putative tumour suppressor protein (RDA32).

Human; cancer; DNA array; gene expression analysis; gene; ss.

Homo sapiens.

JF2002058495-A.

26-FEB-2002.

22-AUG-2000; 2000JP-0255737.

22-AUG-2000; 2000JP-0255737.

(HITA) HITACHI LTD.

WPI; 2002-397522/43.

A DNA array that observes the expression of cancer related genes is useful for the elucidation of the action mechanism of anticancer agents

Disclosure; Page 30; 71pp; Japanese.

CC The invention relates to a DNA array for identifying cancer related
CC genes. The DNA array comprises: (a) statistically significantly higher
CC results of over 10% in homology search of a DNA molecule describing
CC different genes or a complementary DNA (cDNA); (b) statistically
CC significantly higher results (p value) of over 10% in homology search
CC with human Alu sequence; (c) difference of melting temperature of the
CC DNA fragment and hybridisation temperature at 30 degree C or less; (d)
CC the DNA fragment prepared by immobilisation of a DNA short sequence with
CC a specific higher order structure; and (e) the DNA fragment without
CC short repetitive sequence. The array is used in elucidation of the action
CC mechanism of anticancer agents. ABK92989-ABK93090 represent human
CC cancer related genes and associated primers of the invention.

XX Sequence 303 BP, 56 A; 93 C; 117 G; 37 T; 0 other;

Query Match 14.0%; Score 234.4; DB 24; Length 303;

Best Local Similarity 99.6%; Pred. No. 1.1e-49;

Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 CCGGGGCGGTGGTGGCGGCTACGAGCGCGAGACTGGGGGAGCGGCGGTACGGCTAT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 68 CCGGGGCGGTGGTGGCGGCTACGAGCGCGAGACTGGGGGAGCGGCGGTACGGCTAT 127
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 GGGGAGGCGGAGGCGGCTCTTTCGAATGACTGAGAGACGACGACGACGAGCTGTA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 128 GGGGAGGCGGAGGCGGCTCTTTCGAATGACTGAGAGACGACGACGAGCTGTA 187
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 CTGAGCCAGAGAGACTGAGACTGAGACTGAGACTGAGACTGAGACTGAGACTGAGACT 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 188 CTGAGCCAGAGAGACTGAGACTGAGACTGAGACTGAGACTGAGACTGAGACTGAGACT 247
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 181 AGCTGCAAGGCGGCGGCGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 236
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 248 AGCTGCAAGGCGGCGGCGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Search completed: August 20, 2003, 09:41:51
Job time : 510.085 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 02:36:27 ; Search time 4070.96 Seconds
(without alignments)
10029.942 Million cell updates/sec

Title: US-10-023-530-3

Perfect score: 1680
Sequence: 1 ccggggcggtgtgtgctggcgcc.....ccaaaaaaaaaaaaaaaaaa 1680

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_hiv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rnd:*
26: em_gss_ping:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	981.6	58.4	1201	9	AL523074
2	981.2	58.4	1201	9	AL554060
3	977.8	58.1	1000	9	AL579009
4	975.6	58.1	1046	13	BX402736

5	952.4	56.7	1201	9	AL543484	AL543484
6	918.6	54.7	1201	9	AL543447	AL543447
7	916.4	54.5	1201	9	AL554061	AL554061
8	916	54.5	1201	9	AL578918	AL578918
9	914.4	54.4	1050	13	BX344328	BX344328
10	912.8	54.3	1201	9	AL523075	AL523075
11	911.2	54.2	972	9	AL576710	AL576710
12	909.8	54.2	1144	9	AL573913	AL573913
13	896.8	53.4	1201	13	BX385986	BX385986
14	886.8	52.8	1006	9	AL553818	AL553818
15	854.8	50.9	1201	13	BX458932	AL553818
16	854.6	50.9	1126	9	AL549892	BX458932
17	845.4	50.3	920	9	AL560451	AL549892
18	838.8	49.9	1017	12	BM917709	AL560451
19	837	49.8	1054	12	BM451480	BM917709
20	839	49.3	868	12	BT916624	BM451480
21	821.2	48.9	929	13	BX408425	BT916624
22	797.8	47.5	935	9	AL581893	BX408425
23	770.4	45.9	903	13	BQ689604	AL581893
24	768.8	45.8	784	12	BI669331	BQ689604
25	768	45.7	791	13	BU616689	BI669331
26	766.6	45.6	1201	13	BX458933	BU616689
27	766	45.6	906	12	BT664046	BX458933
28	762.2	45.4	846	13	BQ438298	BT664046
29	755.2	45.0	808	12	BI917396	BQ438298
30	752	44.8	918	14	CA489873	BI917396
31	747.2	44.5	797	14	CA503126	CA489873
32	742.2	44.2	934	13	BU860247	CA503126
33	736.2	43.8	764	12	BM051740	BU860247
34	726.6	43.2	907	12	BI913734	BM051740
35	726.4	43.2	778	12	BI762901	BI913734
36	714	42.5	764	10	BG570090	BI762901
37	707.6	42.1	714	12	BM725066	BG570090
38	700	41.7	778	12	BM065590	BM725066
39	684.4	40.7	924	12	BG772022	BM065590
40	670.4	39.9	616	13	BT102498	BG772022
41	669.6	39.9	813	13	BT187947	BT102498
42	667.8	39.8	774	14	CA428454	BT187947
43	665	39.6	687	12	BM981338	CA428454
44	664.6	39.6	1015	12	BM452113	BM981338
45	659.6	39.3	691	12	BM977703	BM452113

ALIGNMENTS

RESULT 1
LOCUS AL523074 1201 bp mRNA linear EST 22-MAY-2003
DEFINITION AL523074 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DC001ygc10 3-PRIME, mRNA sequence.
ACCESSION AL523074
VERSION AL523074.2 GI:31041335
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polyes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12766567.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2262.f FOR
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CS0DC001BD05NP1acluster-2262.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :

OY	672	TTGCAAGAGCCCTAGAGCTTGTCTCGAAGAAATGACTCGGGAGGTGAACCTGGACG	731
Db	962	KTACAAGGCCCTAGCTTGTCTCTGAAGAAATAACTCTGGGGAGGTGAACCTGGACG	903
OY	732	CCCTACAGCATGCCGAACACTACATCTCTACAGTATCTCTACAGCGAGAGAGAGAGC	791
Db	902	CCCTACDGCATGCCGAACACTACATCTCTACAGTATCTCTACAGCGAGAGAGAGAGC	843
OY	792	ACCTCCGCGAGATCCTGCAGAGTACTCTATTGGCCGACAGATCCAGAGGCCCTGC	851
Db	842	ACCTCCGCGAGATCCTGCAGAGTACTCTATTGGCCGACAGATCCAGAGGCCCTGC	783
OY	852	ACGCGTACCCCTTTGGGTGACCTCTGTACCCCGAGGTGAAAGGAGACACAGGCACAGC	911
Db	782	ACGCGTACCCCTTTGGGTGACCTCTGTACCCCGAGGTGAAAGGAGACACAGGCACAGC	723
OY	912	CCAAGTCCGTGCGCGTGTAGTGTACAGAGGCGAGTGGGCCCTGTGGAAATGATGTGAC	971
Db	722	CCAAGTCCGTGCGCGTGTAGTGTACAGAGGCGAGTGGGCCCTGTGGAAATGATGTGAC	663
OY	972	GAGGCCCTCCTGTGTCTGGGGGAATGAGCCACAGAGACAGCAAGTACCTGCTCCCTGTG	1031
Db	662	GAGGCCCTCCTGTGTCTGGGGGAATGAGCCACAGAGACAGCAAGTACCTGCTCCCTGTG	603
OY	1032	TCCACCTATGGGGGTAGCCAGGTATGGCTGACCCCTCTGGCCCTCATTTACTGGGCCCT	1091
Db	602	TCCACCTATGGGGGTAGCCAGGTATGGCTGACCCCTCTGGCCCTCATTTACTGGGCCCT	543
OY	1092	AGTGGGCGAGGGCGCCCTGAGAAGCTCTTCACAGCCCTGCAGCAGAGATGGTGCAGACG	1151
Db	542	AGTGGGCGAGGGCGCCCTGAGAAGCTCTTCACAGCCCTGCAGCAGAGATGGNGCAGACG	483
OY	1152	AAGTCTCCTCAATTTTGTCTCAGAGTGAATACTTGGAGACCCCTGCAACAGAACAGG	1211
Db	482	AAGTCTCCTCAATTTTGTCTCAGAGTGAATACTTGGAGACCCCTGCAACAGAACAGG	423
OY	1212	GTCATGTTGGAGGGGTGACGGCCCTCATCATATAGGAAAGGTTTGGATCTTGAAATGG	1271
Db	422	GTCATGTTGGAGGGGTGACGGCCCTCATCATATAGGAAAGGTTTGGATCTTGAAATGG	363
OY	1272	GTCACAGGATATTCCTATACAGAGCTAAAGGGGTGTCACAAATTAAGCAGAGCATTTGAG	1331
Db	362	GTCACAGGATATTCCTATACAGAGCTAAAGGGGTGTCACAAATTAAGCAGAGCATTTGAG	303
OY	1332	AAGAGCTTGGTTCCTCTACAGTGCACACTCCTCACACACCCTGAGGTACAGGAGTGC	1391
Db	302	AAGAGCTTGGTTCCTCTACAGTGCACACCCTCTCACACACCCTGAGGTACAGGAGGCG	243
OY	1392	TGGCTCACAGACAGCATGTGCCCTAATGCTTCATATAGAGAGATGTCCTGGGCCACAG	1451
Db	242	TGGCTCACAGACAGCATGTGCCCTAATGCTTCATATAGAGAGATGTCCTGGGCCACAG	183
OY	1452	GTCGTGTGATGTGGGCACTGGGCCAGGTCATACCTTAATTTGCTTAATCAAGACGACAG	1511
Db	182	GTCGTGTGATGTGGGCACTGGGCCAGGTCATACCTTAATTTGCTTAATCAAGACGACAG	123
OY	1512	TCTCTCCCTCAGGTGTATTTATGAAAGTGCCTGAATGTATGTAATGTGTGGTGCCTCAG	1571
Db	122	TCTCTCCCTCAGGTGTATTTATGAAAGTGCCTGAATGTATGTAATGTGTGGTGCCTCAG	63
OY	1572	CTGAATGCTCTGTGGGGAAGGGGTTGGGGTGACACTCATCATCAGGCTGGGGG	1628
Db	62	CTGAATGCTCTGTGGGGAAGGGGTTGGGGTAACACTCATCAGGCTGGGGG	6

RESULT 3	AL579009/c	1000 bp	mrna	linear	EST 01-JUN-2003
LOCUS	AL579009				
DEFINITION	AL579009 Homo sapiens HELA CELLS COR 25-NORMALIZED				
ACCESSION	CDNA clone CS00DR012Y101.3-PRIME, mRNA sequence.				
VERSION	AL579009				
KEYWORDS	AL579009.2 GI:31317195				
	EST.				

SOURCE ORGANISM	REFERENCE
Homo sapiens (human)	1, M. B., Gruber, C., Jassee, J. and Polayres, D. Full-length cDNA libraries and normalization
Homo sapiens	1, (bases 1 to 1000)
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.	Unpublished
	On Feb 10, 2001 this sequence version replaced gi:12943631.

For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq-CS00K012AE01NP1&cluster=2262.f>. Contact : Feng Liang Email : liangell@tech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Paraday Avenue Genoscope sequence ID : CS00K012AE01NP1.

FEATURES	Location/Qualifiers
source	1. .1000

BASE COUNT 220 a 308 c 244 g 214 t 14 others

ORIGIN

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODK012Y101"
 /cell_type="HELA CELLS COT 25-NORMALIZED"
 /cell_line="HELA"
 /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match	58.2%	Score 977.8;	DB 9;	Length 1000;
Best Local Similarity	97.8%	Pred. No. 4.6e-159;		
Matches 978; Conservative	11;	Mismatches	0;	Gaps 0

QY	631	GGATGAGAGGCCCGCGGGCTGCGGGCTCCTGGCAGAGGCCAGTGAACAAGGCCCTAGACT	690
Dp	1000	TGAATGAGAGGCCCGCGGGCTGCGGGCTCCTGGCAGGCCCAATGACAAGGCCCTAGACT	941
QY	691	TGTCCTGAAGAAAATGACTCTGGGAGGTGAACCTGAGCGCCTTCAGCATGCTGAAC	750
Dp	940	TGTCCTGAAGAAAATGACTCTGGGAGGTGAACCTGAGCGCCTTCAGCATGCTGAAC	881
QY	751	ACATPACTCTCTAGCTATCTCTGACAGCGGAGAGAGAGACACCTTCGCCAGATCTTGCA	810
Dp	880	ACATPACTCTCTAGCTATCTCTGACAGCGGAGAGAGAGACACCTTCGCCAGATCTTGCA	821
QY	811	GAACTACTCTATTGCGCCGACGAAGATCCAAGAGGCCCTGCAGCGCTGGCCCTTGGGGT	870
Dp	820	GAACTACTCTATTGCGCCGACGAAGATCCAAGAGGCCCTGCAGCGCTGGCCCTTGGGGT	761
QY	871	ACCTCTTTGTACCCCGAGGTGAGAGGACAGACAGCAGCGCAAGTGGCTGCGTGTGA	930
Dp	760	ACCTCTTTGTACCCCGAGGTGAGAGGACAGACAGCAGCGCAAGTGGCTGCGTGTGA	701
QY	931	GTGTGACAGGGCCAGTGGGGCTGTGGAAATGATGGATGGAGGCCCTTCGTGTCGGG	990
Dp	700	GTGTGACAGGGCCAGTGGGGCTGTGGAAATGATGGATGGAGGCCCTTCGTGTCGGG	641
QY	991	GGAAATGAGACCCAGAGAACAGCAAGTACTGCTCCTGTGTGCACCTATGGGTATAGC	1051
Dp	640	GGAAATGAGACCCAGAGAACAGCAAGTACTGCTCCTGTGTGCACCTATGGGTATAGC	581
QY	1051	AGGATATGCTCTGCACCCCTCTGCCCTATTACTGTGGCCTTAGTGGGCCAGGGCTGCCT	1111
Dp	580	AGGATATGCTCTGCACCCCTCTGCCCTATTACTGTGGCCTTAGTGGGCCAGGGCTGCCT	521

OY		1111	GAGAAAGCTGCATCCACAGGCGCTGGCAGCAGAGTGTGTGACACAGAAGCTCCTCAATTTC	1170'
Db		520	GAGAAAGCTGCATCCACAGGCGCTGGCAGCAGAGTGTGTGACACAGAAGCTCCTCAATTTC	461
OY		1171	CTCAGAAAGTAATAATCTTGAGACCCTGCCAACAAGAACAGGATCATGTTTGCAGGGGTGA	1230'
Db		460	CTCAGAAAGTAATAATCTTGAGACCCTGCCAACAAGAACAGGATCATGTTTGCAGGGGTGA	401
OY		1231	CGGCGCCTATCTATGAGGAAGAGTTTGATCTTGAATGTGTCTCAGAGATATCCTTATC	1290'
Db		400	CGGCGCCTATCTATGAGGAAGAGTTTGATCTTGAATGTGTCTCAGAGATATCCTTATC	341
OY		1291	AGAGCTTAAGGGTGGGTGCTCAGAAATTAAGCAGGCGATTGAGAGAGAGTCTTGTTCTCTC	1350'
Db		340	AGAGCTTAAGGGTGGGTGCTCAGAAATTAAGCAGGCGATTGAGAGAGAGTCTTGTTCTCTC	281
OY		1351	TACAGTGGCAACTCTCTCACACACCTTAGAGTGCAGGGAGTCTGGCTCACAGTACAGCATG	1410'
Db		280	TACAGTGGCAACTCTCTCACACACCTTAGAGTGCAGGGAGTCTGGCTCACAGTACAGCATG	221
OY		1411	TGCCTTAATGCTTCATATGAGAGAGATGTCCCTGGCCAGGCTCTGTATGATGTGGGCA	1470'
Db		220	TGCCTTAATGCTTCATATGAGAGAGATGTCCCTGGCCAGGCTCTGTATGATGTGGGCA	161
OY		1471	CTGGCCCCAGGTTCACTACTTATTTGCTATATCAAAGCCAGGCTCTCTCCCTCAGGTGTTT	1530'
Db		160	CTGGCCCCAGGTTCACTACTTATTTGCTATATCAAAGCCAGGCTCTCTCCMAAGGTGTTT	101
OY		1531	TTATGAAGTGGGTAAATATATATATGATGTGTGGCCCTCAGCTGAATCCCTCGTGGGG	1590'
Db		100	TTATGAAGTGGGTAAATATATATATGATGTGTGTGGCCCTCAGCTGAATCCCTCTGTGGGG	41
OY		1591	AAAGGGGTGGGGTGACAGTCATCATCAAGCCCTGGGGCTG	1630'
Db		40	AAAGGGGTGGGGTGACAGTCATCAAAAACAGAGCTGGGMDG	1
RESULT 4				
EX402736/c				
LOCUS	BX402736	1046 bp	mRNA	linear EST 13-MAY-2003
DEFINITION	BX402736 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA			
ACCESSION	clone CSOD1081B21 3-PRIME, mRNA sequence.			
VERSION	BX402736			
KEYWORDS	BX402736.1 GI:30632100			
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
AUTHORS	Homo sapiens			
TITLE	Eumaiyotia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
COMMENT	l1.(bases 1 to 1046) L1.M.B., Gruber,C., Jesse,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2262.f for more information about this cluster, see http://www.genoscope.cns.fr/ cg1-bin/cluster.cgi?seq=CS1A10212B1NP1&cluster=2262.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue genoscape sequence ID : CS1A10212B1NP1.			
FEATURES				
SOURCE	Location/Qualifiers			
	1..1046			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="CSOD1081B21"			
	/cissue_type="PLACENTA COT 25-NORMALIZED"			
	/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"			

Query Match	Best Local Similarity	Score	DB	Length
Matches 983; Conservative 13; Mismatches 15; Indels 1; Gaps 1;	97.1%; Pred. 1.1e-158;	975.6;	13;	1046;
Db	604	CCAAAGTACTACTGCGGAGAGCTGTTGGATGAGAGCAGCAGCCCTGCGCTGCGGCTCTGGC	663	
Db	1046	CCAAGTTACTGTGGGAGAGCTKTTGGATGATGAGCAGCCCTGCGGCTGCGGCTCTGGC	987	
Db	664	AGGCGCCAGTGACAAAGCCCTGAGCTTTGTCTCTGAAGAAATGACTCTGGGAGGTGA	723	
Db	986	AGGGGCCAKKTACAAAGGCCCTGAGCTTTKCTCTGAAGAAATGACTCTGGGAGGTGA	927	
Db	724	CTGGAGACCTCTTTCAGCATGCTGAACTCATATACCTTCTAGGTATCCCTGACGGGAGGA	783	
Db	926	CTGGAGACCTCTTTCAGCATGCTGAACTCATATACCTTCTAGGTATCCCTGACGGGAGGA	867	
Db	784	GGAGAGACACTCGCCGACATCTCTGACAGAGTACTCTTATTTCCGCCGCAAGATCCAGA	843	
Db	866	GGAGAGACACTCGCCGACATCTCTGACAGAGTACTCTTATTTCCGCCGCAAGATCCAGA	807	
Db	844	GGCCCTGACAGCCCTGCGCCCTTGGGTGACCTTTGTATCCGCCAGGTGGAAGGACAGC	903	
Db	806	GGCCCTGACAGCCCTGCGCCCTTGGGTGACCTTTGTATCCGCCAGGTGGAAGGACAGC	748	
Db	904	AGGCAGGCCCAAGTGCCTGCGCTGTGATGTGACAGGGCCAGTGGGGCTGTGAAATAG	963	
Db	747	AGGCAGGCCCAAGTGCCTGCGCTGTGATGTGACAGGGCCAGTGGGGCTGTGAAATAG	688	
Db	964	TGTGATGAGGAGCCCTCTCTGATGCGGGGAGATGAGCCGAGAAACAGGAAGTACTGTC	1023	
Db	687	TGTGATGAGGAGCCCTCTCTGATGCGGGGAGATGAGCCGAGAAACAGGAAGTACTGTC	628	
Db	1024	TCCCTGTCTCACACTATAGGTGTGTAGCCAGTATGGCTTGCACCCCTTGCCTCATATAC	1083	
Db	627	TCCCTGTCTCACACTATAGGTGTGTAGCCAGTATGGCTTGCACCCCTTGCCTCATATAC	568	
Db	1084	TGGGCTTATGTGGGCGCAGGGCTGCCCTGAGAACTGCTCCAGGCTGACAGAGTGT	1143	
Db	567	TGGGCTTATGTGGGCGCAGGGCTGCCCTGAGAACTGCTCCAGGCTGACAGAGTGT	508	
Db	1144	GCAGACAGAAATCTCCCAATTTTTTGTCTGAAAGTGAATCTTTGGAGACCCGTGCAAC	1203	
Db	507	GCAGACAGAAATCTCCCAATTTTTTGTCTGAAAGTGAATCTTTGGAGACCCGTGCAAC	448	
Db	1204	AGAA-CAGGCTATGTTG-CAGGGGTGAGCGGCTCATCTATAGAGAAAGTTTGGATCT	1263	
Db	447	AGAA-CAGGCTATGTTG-CAGGGGTGAGCGGCTCATCTATAGAGAAAGTTTGGATCT	388	
Db	1264	TGAATGTGCTCAGAGATATCCTTATACAGACTTAAGGTTGGGTCTCAGATTAARACAGG	328	
Db	387	TGAATGTGCTCAGAGATATCCTTATACAGACTTAAGGTTGGGTCTCAGATTAARACAGG	328	
Db	1324	CATTGAGGAAGAGTCTGGTTTCTCTACAGTGCACAACTCCTCACAACCCCTGAGTCA	1383	
Db	327	CATTGAGGAAGAGTCTGGTTTCTCTACAGTGCACAACTCCTCACAACCCCTGAGTCA	268	
Db	1384	GGGAGTCTGGCTCACAAGTATACAGATATGCTTATATGAGAGAGATGTCCCT	1443	
Db	267	GGGAGTCTGGCTCACAAGTATACAGATATGCTTATATGAGAGAGATGTCCCT	208	
Db	1444	GGGAGTCTGGCTCACAAGTATGAGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT	1503	
Db	207	GGGAGTCTGGCTCACAAGTATGAGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT	148	
Db	1504	AGCCAGGCTCTCTCCCTCAGGCTGTTTTTATGAAGTCCGGAATGTATGATGTGTGT	1563	

Db 147 AGCCAGAGTCTCTCCCTCAGGTGTTTATATAGAGTGAATGTATGTATGTGT 88

QY 1564 GGCCTCAGCTGAATGCTCTCTCTGGGGAAGGGGTTGGGATGACAGTCA 1615
 |||||
 Db 87 GGCCTCAGCTGAATGCTCTCTCTGGGGAAGGGGTTGGGATGACAGTCA 36

RESULT 5
 AL543484
 LOCUS
 DEFINITION AL543484 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1003YK08 5-PRIME, mRNA sequence.
 AL543484
 VERSION AL543484.2 GI:31265331
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 JOURNAL Full-length cDNA libraries and normalization
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12875962.
 Contact: Genoscope
 Genoscope - Centre National de Sequençage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 2262.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1003BF04QPI&cluster=2262.f. Contact :
 Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D1003BF04QPI.

FEATURES
 source Location/Qualifiers
 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1003YK08"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 266 a 263 c 338 g 283 t 51 others

ORIGIN

Query Match 56.7% Score 952.4; DB 9; Length 1201;
 Best Local Similarity 97.2% Pred. No. 1e-154;
 Matches 962; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 691 TGTCTGAAGAAATGACTGTGGGAGGTGAAGTGGAGCGCTTCAGCATGCTGA 750
 |||||
 Db 66 TGTCTGAAGAAATGACTGTGGGAGGTGAAGTGGAGCGCTTCAGCATGCTGA 125

QY 751 ACATACTCTCTACGATCTCTGACGGGAGAGAGACACCTCCGACAGTCTGCA 810
 |||||
 Db 126 ACATACTCTCTACGATCTCTGACGGGAGAGAGACACCTCCGACAGTCTGCA 185

QY 811 GAAGTACTCTCTATGCGCCAGAGATCCAGAGCGCCGACGCTGGCCCTGGGG 870
 |||||
 Db 186 GAAGTACTCTCTATGCGCCAGAGATCCAGAGCGCCGACGCTGGCCCTGGGG 245

QY 871 ACCTCTTGATCCCGCAGGTGAAGGACAGACAGCAGCGCCCAAGTGGTGGCTGTGA 930
 |||||
 Db 246 ACCTCTTGATCCCGCAGGTGAAGGACAGACAGCAGCGCCCAAGTGGTGGCTGTGA 305

QY 931 GTGTGACAGGCGCAGTGGGGCTGTGGAATGAGTGCATGGAGCCCTCTGTGCTGG 990
 |||||

Db 306 GTGTGACAGGCGCCAGTGGGGCTGTGGAATGAGTGCATGGAGGCCCTCTGTGCTGG 365

QY 991 GGAATAGGCCCAAGAGAAGCAGGAAGTGTGCTGCTCCCTGTGTCACCTATGGGTAGCC 1050
 |||||
 Db 366 GGAATAGGCCCAAGAGAAGCAGGAAGTGTGCTGCTCCCTGTGTCACCTATGGGTAGCC 425

QY 1051 AGGTATGGCTGTGACACCCCTGTGCTCATTTACTGAGGCTTATGGGCCAGGGCTGCC 1110
 |||||
 Db 426 AGGTATGGCTGTGACACCCCTGTGCTCATTTACTGAGGCTTATGGGCCAGGGCTGCC 485

QY 1111 GAGAACCTCTCCAGGCCCTGACAGAGAGTGTGACAGAGAGTCTCTCAATTTTGT 1170
 |||||
 Db 486 GAGAACCTCTCCAGGCCCTGACAGAGAGTGTGACAGAGAGTCTCTCAATTTTGT 545

QY 1171 CTCAGAGTGAATAATTGTGAGACCTGCAACAGAGAGGTCATGTTTGCAGGGGTGA 1230
 |||||
 Db 546 CTCAGAGTGAATAATTGTGAGACCTGCAACAGAGAGGTCATGTTTGCAGGGGTGA 605

QY 1231 CGGCCCTCATATGAGGAAAGGTTTGGATCTTGAATGTGTCTCAGATATCTTATC 1290
 |||||
 Db 606 CGGCCCTCATATGAGGAAAGGTTTGGATCTTGAATGTGTCTCAGATATCTTATC 665

QY 1291 AGAGCTAAGGTTGGTGTCTCAGATATGAGGAGCATTTGAGAAAGTCTTGTCTCTC 1350
 |||||
 Db 666 AGAGCTAAGGTTGGTGTCTCAGATATGAGGAGCATTTGAGAAAGTCTTGTCTCTC 725

QY 1351 TACAGTGAACCTCTCAGACACCCAGAGTGCAGAGTGCCTGACAGTACAGATG 1410
 |||||
 Db 726 TACAGTGAACCTCTCAGACACCCAGAGTGCAGAGTGCCTGACAGTACAGATG 785

QY 1411 TGCCTTAATGCTTCATATGAGAGAGATGTCCCTGAGGCTGTGTGAATGTGGGA 1470
 |||||
 Db 786 TGCCTTAATGCTTCATATGAGAGAGATGTCCCTGAGGCTGTGTGAATGTGGGA 845

QY 1471 CTGGCCCAAGTGTATACCTTATTTGCTATCAAGCAGGCTCTCTCAGAGTCTTT 1530
 |||||
 Db 846 CTGGCCCAAGTGTATACCTTATTTGCTATCAAGCAGGCTCTCTCAGAGTCTTT 905

QY 1531 TTATGAGTGCCTGATATGATGTATGTGTGTGGCTCAGTGAATGCTCTGTGGG 1590
 |||||
 Db 906 TTATGAGTGCCTGATATGATGTATGTGTGTGGCTCAGTGAATGCTCTGTGGG 965

QY 1591 AAAGGTTGGGTGACAGTCAATCAGGCTGGGCTGAGAAATTTGGCTCAATTAAG 1650
 |||||
 Db 966 AAAGGTTGGGTGACAGTCAATCAGGCTGGGCTGAGAAATTTGGCTCAATTAAG 1025

QY 1651 ATTTCAGATCAAAAAAAAAAAAAAAAAAAAA 1680
 |||||
 Db 1026 TTTAAGATCCCTCAAAAAAAAAAAAAAAAAAAAA 1055

RESULT 6
 AL543447/c 1201 bp mRNA linear EST 31-MAY-2003
 LOCUS AL543447 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1003YK08 3-PRIME, mRNA sequence.
 AL543447
 VERSION AL543447.2 GI:31265294
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 JOURNAL Full-length cDNA libraries and normalization
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12875925.
 Contact: Genoscope
 Genoscope - Centre National de Sequençage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2262.f. For more information about this cluster, see

<http://www.genoscope.cns.fr/cgl-bin/cluster.cgi?seq=CSOD1003BF04NP1cluster=2262.f>. Contact : Feng Liang Email : liang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSOD1003BF04NP1.

FEATURES

source

```

1.1201
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1003YK08"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      269 a      303 c      275 g      268 t      86 others
ORIGIN

```

Query Match 54.7% Score 918.6; DB 9; Length 1201;

Best Local Similarity 97.3% Pred. No. 7.1e-149;

Matches 926; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

```

691 TGTCTGAAGGAAATGACTCTGGGAGAGTGAATCGGACGCTTACAGATGCTGAAGT 750
|||||
954 TGTCTGAAGGAAATGACTCTGGGAGAGTGAATCGGACGCTTACAGATGCTGAAGT 895
|||||
751 ACATTAATCTTCTAGCTATCTGCAGCGGAGAGAGGACGCTCCGCGAGATCTTCA 810
|||||
894 ACATTAATCTTCTAGCTATCTGCAGCGGAGAGAGGACGCTCCGCGAGATCTTCA 835
|||||
811 GAAGTACTCTTATTCGCGCAGAAAGATCCAAAGAGGCGCTGACGCGCTTGGGTTG 870
|||||
834 GAAGTACTCTTATTCGCGCAGAAAGATCCAAAGAGGCGCTGACGCGCTTGGGTTG 775
|||||
871 ACCCTTGTACCCCGAGGTGGAAGGACAGACAGGAGCGCCGAAGTGGCTGCTGCA 930
|||||
774 ACCCTTGTACCCCGAGGTGGAAGGACAGACAGGAGCGCCGAAGTGGCTGCTGCA 715
|||||
931 GTGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 990
|||||
714 GTGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 655
|||||
991 GGAATGAGCCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1050
|||||
654 GGAATGAGCCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 595
|||||
1051 AGATATGGCTCTGCAGCCCTTGCCTTATTAAGGAGGAGGAGGAGGAGGAGGAGG 1110
|||||
594 AGATATGGCTCTGCAGCCCTTGCCTTATTAAGGAGGAGGAGGAGGAGGAGGAGG 535
|||||
1111 GAGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1170
|||||
534 GAGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 475
|||||
1171 CTGGAAGTGAATTTCTTGAAGACCTTGCACAAAGAGGAGGAGGAGGAGGAGGAG 1230
|||||
474 CTCGAAGTGAATTTCTTGAAGACCTTGCACAAAGAGGAGGAGGAGGAGGAGGAG 415
|||||
1231 CGGCGCTCATATGAGGAAAGGTTTGGATCTTGAATGTTGCTCAGAGATATCTTATC 1290
|||||
414 CGGCGCTCATATGAGGAAAGGTTTGGATCTTGAATGTTGCTCAGAGATATCTTATC 355
|||||
1291 AGAGCTAAGGGTGGGTGCTCAGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1350
|||||
354 AGAGCTAAGGGTGGGTGCTCAGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 295
|||||
1351 TACAGTGCACACTCTCTACACACCCCTGAGTCAAGGAGTGTGGCTCAGATACAGATG 1410
|||||
294 TACAGTGCACACTCTCTCTACACACCCCTGAGTCAAGGAGGAGGAGGAGGAGGAG 235
|||||

```

```

QY 1411 TGCCTTAATGCTTCATATGAGAGGATGTCCTGGGCGAGGCTGTGTGAATGTGGCA 1470
|||||
DB 224 TGCCTTAATGCTTCATATGAGAGGATGTCCTGGGCGAGGCTGTGTGAATGTGGCA 175
|||||
QY 1471 CTGGGCGAGGTCATACCTTTATTTCTTATTAAGGAGGAGGAGGAGGAGGAGGAGG 1530
|||||
DB 174 CTGGGCGAGGTCATACCTTTATTTCTTATTAAGGAGGAGGAGGAGGAGGAGGAGG 115
|||||
QY 1531 TTATGAAGTGCCTGAATGATATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1590
|||||
DB 114 TTATGAAGTGCCTGAATGATATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 55
|||||
QY 1591 AAAGGGTTGGGTTGAGCAGTATCATTCAGGCGCTGGGCTGAGAGATTTGGCT 1642
|||||
DB 54 AAAGGGTTGGGTTGAGCAGTATCATTCAGGCGCTGGGCTGAGAGATTTGGCT 3
|||||

```

RESULT 7

AL554061

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On Feb 15, 2001 this sequence version replaced gi:12894483.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2262.f. For

more information about this cluster, see

<http://www.genoscope.cns.fr/cgl-bin/cluster.cgi?seq=CSOD1081C1A110P1cluster=2262.f>. Contact :Feng Liang Email : liang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CSOD1081C1A110P1.

Location/Qualifiers

1.1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSOD1081YB21"

/issue_type="PLACENTA COT 25-NORMALIZED"

/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT

250 a

330 c

356 g

230 t

35 others

ORIGIN

Query Match

54.5% Score 916.4; DB 9; Length 1201;

Best Local Similarity 92.0% Pred. No. 1.7e-148;

Matches 997; Conservative 30; Mismatches 49; Indels 8; Gaps 6;

```

QY 1 CCGGGGCGGTGTTGGGCTACGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
|||||
DB 121 CCGGGGCGGTGTTGGGCTACGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
|||||
QY 61 GGGGAGGCGGAGGCGGCTTCTTGAATGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAG 120
|||||
DB 181 GGGGAGGCGGAGGCGGCTTCTTGAATGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAG 240
|||||

```

OY	121	TTGAGCCCAAGAGACTGCGAGCTGCGAGCTGAGACAGTACTTCAACCGGGCAACCTGGCT	180
Db	241	CTGCGACCCAAAGAGACTGCGAGCTGCGAGCTGAGACAGTACTTCAACCGGGCAACCTGGCT	300
OY	181	AGCTCGACGAGCGCGCGGACCAAGAGAGAGAGCTGTGGAGTGGGAGACACCTGACTTTC	240
Db	301	AGCTCGACGAGCGCGCGGACCAAGAGAGAGCTGTGGAGTGGGAGACACCTGACTTTC	360
OY	241	TCAAGCTGAGATTGAGCAGAAATCAGAGAGTACATGCCAGATCAACAGCAACTCTT	300
Db	361	TCAAGCTGAGATTGAGCAGAAATCAGAGAGTACATGCCAGATCAACAGCAACTCTT	420
OY	301	CATAGAGCTGAACAAGGACGGTTCTTACAGAGGCTTCAACAGGTTGACGTGAAGCTGGT	360
Db	421	CATAGAGCTTGAACAAGGACGGTTCTTACAGAGGCTTCAACAGGTTGACGTGAAGCTGGT	480
OY	361	GCGCCCTGTCTGTGCCCTCCAGACAGAACCCCTCTTGCAGATGCCCCGGCGGG	420
Db	481	GCGCCCTGTCTGTGCCCTCCAGACAGAACCCCTCTTGCAGATGCCCCGGCGGG	540
OY	421	CCCGAGACGGGGCACAAAGTGTCAAGGCGCGCACTTCTTTAACTGCCCCAAGATGCTGT	480
Db	541	CCCGAGAGGGGGCACAAAGTGTCAAGGCGCGCACTTCTTTAACTGCCCCAAGATGCTGT	600
OY	481	CAACACACCTGCATGTGCTGCAGCAGACAAAGGGACAGTAAATCATTTGAGGCGCTGTCG	540
Db	601	CAACACACCTGCATGTGCTGCAGCAGACAAAGGGACAGTAAATCATTTGAGGCGCTGTCG	659
OY	541	AAAGTTCTTGGTGTGATGACCCCGCAATTTGCACTCTTGAAGCGCTGAGCTCA	600
Db	660	AAAGTTCTTGGTGTGATGACCCCGCAATTTGCACTCTTGAAGCGCTGAGCTCA	719
OY	601	CGGCGAAGTACTGTCGGGAGCGTG-ATTGATGATGAGACACCCCTGCGGCTGCGGCTCC	659
Db	720	CGGCGAAGTACTGTCGGGAGCGTG-ATTGATGATGAGACACCCCTGCGGCTGCGGCTCC	779
OY	660	TGGCAGGGCCCAAGTACAAAGGCGCTGTGCTTGAAGAAATGACTCTGGGGAGG	719
Db	780	TGGCAGGGCCCAAGTACAAAGGCGCTGTGCTTGAAGAAATGACTCTGGGGAGG	839
OY	720	TGAACCTGGAGCCCTTACAGATGCCCTGACATTAACCTCTTACAGTACTCTGACGGGG	779
Db	840	TGAACCTGGAGCCCTTACAGATGCCCTGACATTAACCTCTTACAGTACTCTGACGGGG	899
OY	780	AGGAGGAGGACACCTCGCCAGATTCGCGAAGTACTCCTATGCGCGCAGAAATTC	839
Db	900	AGGAGGAGGACACCTCGCCAGATTCGCGAAGTACTCCTATGCGCGCAGAAATTC	959
OY	840	AAGAGGCGCTCAGCGCTGCCCC-TTGGGTAGACTCTTGTACCCCAAGTGAAGCGAG	898
Db	960	AAGAGGCGCTCAGCGCTGCCCC-TTGGGTAGACTCTTGTACCCCAAGTGAAGCGAG	1019
OY	899	ACACAGGACGCGCCAAAGTGCCTGCTGTAGTGTGACAGAGGCCAGTGGGCGCTGTGGA	958
Db	1020	AAACACAGGACGCGCCAAAGTGCCTGCTGTAGTGTGGAAGGGGAGTTGGGCGCTGTG	1079
OY	959	ATGAGTGTGATGAGGCGCCCTGTGTGTGGGGGAATGAGGCCAGAGAAACGCGAAGTGA	1018
Db	1080	AATGATTTTCAATKAGGCCCT-CTKTCTTGGGGGAATTAACCAAAAACCT- -GGAANA	1133
OY	1019	CTTGCTCCCTGTGTCAACCTATGGAGTGTAGCCAGGATATGGCTGTGACCCCTGTGCTC	1078
Db	1137	CTTGCTCCCTGT	1198
OY	1079	ATTA 1082	
Db	1195	ATKD 1198	

DEFINITION	ACCESSION	VERSION	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
AL578918 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens AL578918 clone CSDDK005YX06 3-PRIME, mRNA sequence.	AL578918	AL578918.2	GI:31317106 EST.	Homo sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (Bases 1 to 1201)	Ll,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization unpublished	On Feb 16, 2001 this sequence version replaced gi:1293453.	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr Library was constructed by life technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2262.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSDDK005BF03NP1&cluster=2262.f. Contact : Feng Liang Email : liliang@life.techn.com URL : http://fulllength.invitrogen.com / invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSDDK005BF03NP1. Location/Qualifiers 1..1201

```

/organism="Homo sapiens"
/mol_type="RNA"
/db_xref="taxon:9606"
/clone="CSODK005YK06"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_1lb="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with NotI and cloned into the NotI and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      263 a      354 c      261 g      243 t      80 others
ORIGIN

```

LOCUS	1201 bp	mRNA	linear	EST
AL578918				01-JUN-2003

Query Match	54.5%	Score 916	DB 9	Length 1201
Best Local Similarity	97.2%	Pred. No. 2e-148		
Matches 95	Conservative	7	Mismatches 10	Indels 3
			Gaps	3
QY	631	TGATGAGCAGCCCTGCGGCTCGGCTCCTGGCAGGGGCCAGTACAGAGCCCTGACCTT	6300	
		..		
Db	1022	TGATGTATGACAGCCCTCGGCTGCGCTCTCTGACR -GGCCCAATGACARGGCGTGACCTT	9640	
QY	691	TGTCCTGAGAGAAATGACTCTGGGAGGTGTAACCTGGGACCCCTTCAGACACCTGTGAACCT	7500	
Db	963	TGTCCTGAGAGAAATGACTCTGGGAGGTGTAACCTGGGACCCCTTCAGACACCTGTGTGAACCT	9050	
QY	751	ACATAACTCTCTACGATCCTGCAGCGGAGGAGGAGGACACCTCGCCAGATCTGCA	8100	
Db	904	ACATAACTCTCTACGATCCTGCAGCGGAGGAGGAGGACACCTCGCCAGATCTGCA	8450	
QY	811	GAAGTACTCCTATGTGCGCCAGACAGT -CCAGAGGCCCTGCACGCTGCCCCCTTGGGT	8650	
Db	844	GAAGTACTCCTATGTGCGCCAGACAGTCCCAAGAGGCCCTGCACGCTGCCCCCTTGGGT	7850	
QY	870	GACCTCTTGTACCCCGCAGGTGGAGGACAGCAGGAGGCCAAGTGGCTGCGGTG	9250	
Db	784	GACCTCTTGTACCCCGCAGGTGGAGGACAGCAGGAGGCCAAGTGGCTGCGGTG	7250	
QY	930	AGTGTGACAGGGCCAGTGGGCCCTGTGGAATGAGTGTCAATGAGAGGCCCTCTGTGTG	9890	
Db	724	AGTGTGACAGGGCCAGTGGGCCCTGTGGAATGAGTGTCAATGAGAGGCCCTCTGTGTG	6650	
QY	990	GGGAATGAGCCCAAGAACAGCAGAGTACTTCTCTGTGTCACTTATGAGGTGAC	1040	
Db	664	GGGAATGAGCCCAAGAACAGCAGAGTACTTCTCTGTGTCACTTATGAGGTGAC	6050	

OY		1050	CAGGATATGGCTTCGTGCACCCCTTGGCCCATATTACTTGAGGGCCTTAGGGGCCAAGGGCTGGCC	1109
OY		604	CAGGATATGGCTTCGTGCACCCCTTGGCCCATATTACTTGAGGGCCTTAGGGGCCAAGGGCTGGCC	545
OY		1110	TGAGAAGCTGCTCGAGGCTGCAGCAGAGAGTGCTGCAGACAGAACTCTCTCAATTTTGG	1169
Db		544	TGAGAAGCTGCTCGAGGCTGCAGCAGAGAGTGCTGCAGACAGAACTCTCTCAATTTTGG	485
OY		1170	TCTCAGAAAGTGAATACTTTGGAGACCCTTCGCAACAGAACAGGGCTCATGTTTTGCAGGGGTG	1229
OY		484	TCTCAGAAAGTGAATACTTTGGAGACCCTTCGCAACAGAACAGGGCTCATGTTTTGCAGGGGTG	425
OY		1230	ACGGCCCTCATCTATGAGAGAAAAGTTTGGAACTTGAAATGTGTGCTCAGATATCCTTAT	1289
Db		424	ACGGCCCTCATCTATGAGAGAAAAGTTTGGAACTTGAAATGTGTGCTCAGATATCCTTAT	365
OY		1230	CAGAGCTTAAGGGTGGGTCTCTCAGAAATAAGCAGACGATTGAGAGAAAGTCTTGTTCTCT	1348
Db		364	CAGAGCTTAAGGGTGGGTCTCTCAGAAATAAGCAGACGATTGAGAGAAAGTCTTGTTCTCT	305
OY		1350	CTACAGTGTCCAACCTCTCACACACCCTGAGGTGAGGGAGTGTGCTGCACAGTACAGCAT	1409
Db		304	CTACAGTGTCCAACCTCTCACACACCCTGAGGTGAGGGAGTGTGCTGCACAGTACAGCAT	245
OY		1410	GTCGCTTAATGCTTCATATATGAGAGAGATGTCCTGGGGCAGAGGTCTGTGAATGTGGGC	1468
Db		244	GTCGCTTAATGCTTCATATATGAGAGAGATGTCCTGGGGCAGAGGTCTGTGAATGTGGGC	185
OY		1470	ACTGGCCCCAGGTCTCATACCTTATTTGCTAAATCAAACCCAGGGTCTCTCCCTCAGGTGTT	1528
Db		184	ACTGGCCCCAGGTCTCATACCTTATTTGCTAAATCAAACCCAGGGTCTCTCCCTCAGGTGTT	125
OY		1530	TTTATGAAGTGCAGTCAATGTATGTAAATGTGTGGGGCTCAGCTGAATGCTCCTGTGG	1589
Db		124	TTTATGAAGTGCAGTCAATGTATGTAAATGTGTGGGGCTCAGCTGAATGCTCCTGTGG	65
OY		1590	GAAAGGGGTTGGGGTGACATCA 1612	
Db		64	GAAAGGGGTTGGGGTGACATCA 42	
RESULT 9				
BX344328				
LOCUS		BX344328	Homo sapiens PLACENR7A.COT 25-NORMALIZED Homo.sapiens cDNA	
DEFINITION			clone CS001081YB21 5-PRIME, mRNA sequence.	
ACCESSION		BX344328		
VERSION		BX344328.1	GI:30309092	
KEYWORDS		EST,		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE		1 (bases 1 to 1050)		
JOURNAL		L1,W.B., Gruber,C., Jessee,J. and Polayes,D.		
COMMENT		Full-length cDNA libraries and normalization		
		Unpublished		
		Contact: Genoscope		
		Genoscope - Centre National de Sequences		
		BP 191 91006 Evry cedex - France		
		Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr		
		Library was constructed by Life Technologies, a division of		
		Invitrogen. This sequence belongs to sequence cluster 2262.f For		
		more information about this cluster, see		
		http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq-CSIAI021ZB1I0P1		
		fcluster=2262.f. Contact : Feng Liang Email : fliang@lifetech.com		
		URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600		
		Fairway Avenue Genoscope sequence ID : CSIAI021ZB1I0P1.		
		Location/Qualifiers		
FEATURES		1..1050		
source		/organism='Homo sapiens'		
		/mol_type='mRNA'		

Query Match	Best Local Match	Similarity	Score	DB	Length
923; Conservative	99.2%; Pred. No. 1; Indels 1; Gaps 1	54.48; Score 914.4; DB 13; Length 1050;			
1	CCGGGGCGGGGTTGGCGGCTACGAGACGGGAGACTGGGGGACGGGGGGTACGGGCTAT	60			
121	CCGGGGCGGCTGTTGGCGGCTACGAGACGGGAGACTGGGGGACGGGAGGTTACGGCTAT	180			
61	GGGCGAGCGGAGGCGGCTTTCTTTCGAAATGACCTGGAGACAGACAGAGAGCTGGCTTA	120			
181	GGGCGAGCGGAGGCGGCTTTCTTTCGAAATGACCTGGAGACAGACAGAGAGCTGGCTTA	240			
121	CTGAGCGCAAGAGAGACTCGGAGCTCGAGAGCTCGAGAGCTACTTACCGGGCCAACTGGCT	180			
241	CTGAGCGCAAGAGAGACTCGGAGCTCGAGAGCTCGAGAGCTACTTACCGGGCCAACTGGCT	300			
181	AGCTCGCAGGCGCGCGCGCGGAGCAGAGAGAGCTGTGAGTGGAGAGACAGCTGACTTTC	240			
301	AGCTCGCAGGCGCGCGCGCGGAGCAGAGAGAGCTGTGAGTGGAGAGACAGCTGACTTTC	360			
241	TCAAGCTGAATTGAGCAGAAAGATCAAGAGATCAATGCCAGATCAACAGCAACTCTT	300			
361	TCAAGCTGAATTGAGCAGAAAGATCAAGAGATCAATGCCAGATCAACAGCAACTCTT	420			
301	CATGAGCTTGAACAGAGAGCTTCTTACAGAGCTTCAATCAAGTTCAGCTGAAGCTGGT	360			
421	CATGAGCTTGAACAGAGAGCTTCTTACAGAGCTTCAATCAAGTTCAGCTGAAGCTGGT	480			
361	GCGCCCTGTCTGTGCGCTCCAGCAAGAGCCACTTCTTACAGAGTGGCGCGCGGG	420			
481	GCGCCCTGTCTGTGCGCTCCAGCAAGAGCCACTTCTTACAGAGTGGCGCGCGGG	540			
421	CCCGAGAGCGGGGACAAAGTGTGAGGGCGGCACTTCTTACCTGGCCCAAGATGCTGT	480			
541	CCCGAGAGCGGGGACAAAGTGTGAGGGCGGCACTTCTTACCTGGCCCAAGATGCTGT	600			
481	CAGACACCTCATGTGCTGTCAAGCAGAGGGCAGCTGAGTCAATTTGAGGCGCTGTGCG	540			
601	CAGACACCTCATGTGCTGTCAAGCAGAGGGCAGCTGAGTCAATTTGAGGCGCTGTGCG	660			
541	AAAGTTCTTGTGCTGTGATGACCCCGCAAGTTTGACCTTTGAGCGCGCTGAGCTCA	600			
661	AAAGTTCTTGTGCTGTGATGACCCCGCAAGTTTGACCTTTGAGCGCGCTGAGCTCA	720			
601	CGGCGCAAGTGTGCTGTGAGTGTGATGATGAGAGCCCGCGCGCTGTGCGCTGT	660			
721	CGGCGCAAGTGTGCTGTGAGTGTGATGATGAGAGCCCGCGCGCTGTGCGCTGT	780			
661	GGCAGGCGCGCAAGTGTGAGTGTGATGATGAGTGTGATGAGTGTGAGTGTGAGTGT	720			
781	GGCAGGCGCGCAAGTGTGAGTGTGATGATGAGTGTGATGAGTGTGAGTGTGAGTGT	840			
721	GAACCTGGAGAGCTTTCAGCATGCTGAGTCAATATTAATCTTCAGTATTCCTGAGCGGGA	780			
841	GAACCTGGAGAGCTTTCAGCATGCTGAGTCAATATTAATCTTCAGTATTCCTGAGCGGGA	900			
781	GAGAGAGAGACACCTCCGAGATCTCTGAGAAAGTACTCTATTGCGCGCAAGATCCA	840			
901	GAGAGAGAGACACCTCCGAGATCTCTGAGAAAGTACTCTATTGCGCGCAAGATCCA	960			
841	AGAGGCGCTGTGACGCTGCGCTTGGGTGATCTTTGTACCCCGAGGTGAGGAGAC	900			

Db 961 AGAGCCCTGACACGCTTGGGTTGACCTTTGTA-CCCCAGGTGGAGGCGAGAM 1019

QY 901 AGACGACGACGCCCAAGTCGTGCCGTGTGA 930

Db 1020 AACGAGCARGCGMAAGTGTGCTGCTGTGA 1049

RESULT 10

AL523075 1201 bp mRNA linear EST 22-MAY-2003

LOCUS AL523075 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens

DEFINITION cDNA clone CS0DC001G10 5-PRIME, mRNA sequence.

ACCESSION AL523075

VERSION AL523075.2 GI:31041336

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT On Feb 13, 2001 this sequence version replaced gi:12786568.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by life technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2262.f for more information about this cluster, see

http://www.genoscope.cns.fr/

cg1-bln/cluster.cgi?seq=CS0DC001BD05QPl&cluster=2262.f. Contact : Feng Liang Email : fliang@life.techn.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DC001BD05QPl.

FEATURES

Source

1..1201

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DC001G10"

/issue_type="NEUROBLASTOMA COT 25-NORMALIZED"

/clone_11b="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 271 a 325 c 355 g 219 t

ORIGIN

Query Match 54.3%; Score 912.8; DB 9; Length 1201;

Best Local Similarity 98.2%; Pred. No. 7,1e-148;

Matches 951; Conservative 3; Mismatches 10; Indels 4; Gaps 3;

QY 1 CCGGGGGCGGTGTGGCGGTACGACCGCGAGCTGGGGAGCGGGGTACGGCTAT 60

Db 102 CCGGGGGCGGTGTGGCGGTACGACCGCGAGCTGGGGAGCGGGGTACGGCTAT 161

QY 61 GGGCGAGCGGAGGGGCGCTTCTTTCGAATGACC-TGGAGCAGCAGCAGCAGCAGTGGCT 119

Db 162 GGGCGAGCGGAGGGGCGCTTCTTTCGAATGACATGGAGCAGCAGCAGCAGTGGCT 221

QY 120 ACTGAGCGCAAGAGGACTCGAGCTCGAGCTCGAGCAGTCTTCAACCGCGGCAACCTGC 179

Db 222 ACTGAGCGCAAGAGGACTCGAGCTCGAGCTCGAGCAGTCTTCAACCGCGGCAACCTGC 281

QY 180 TAGCTCGAGCGCGCGCGG-GACCAGAGCAGCCTGTGTGAGTGGAGAGACACCTGACTT 238

Db 282 TAGCTCGAGCGCGCGCGGNGACAGGAGCAGCCTGTGTGAGTGGAGAGACACCTGACTT 341

QY 239 TCTCAAGCTGAGATTGAGCAGAGATCAAGAGTACATGCCCAATCAACAGCAACCTC 298

Db 342 TCTCAAGCTGAGATTGAGCAGAGATCAAGAGTACATGCCCAATCAACAGCAACCTC 401

QY 299 TCTCATGAGCTTGAACAAGAGCGTTCTTACACAGGCTTATCATAGATTACGTGAAGCTG 358

Db 402 TCTCATGAGCTTGAACAAGAGCGTTCTTACACAGGCTTATCATAGATTACGTGAAGCTG 461

QY 359 GTGGCGCTGTCTGTGTGCGCTTCACAGCAAGAACCCCTCTTCAGAGATCCCGGCGG 418

Db 462 GTGGCGCTGTCTGTGTGCGCTTCACAGCAAGAACCCCTCTTCAGAGATCCCGGCGG 521

QY 419 GGGCCAGAGCGGGGCGCAGAGTGTCAAGGCGCCGCTCTCTTTACTGCTCCCAAGATGCT 478

Db 522 GGGCCAGAGCGGGGCGCAGAGTGTCAAGGCGCCGCTCTCTTTACTGCTCCCAAGATGCT 581

QY 479 GTCAAGCACCTCATGTGCTGTACAGCAGCAAGGGGCGGGAAGTATTGAGGCGCGTGC 538

Db 582 GTCAAGCACCTCATGTGCTGTACAGCAGCAAGGGGCGGGAAGTATTGAGGCGCGTGC 641

QY 539 CGAAGTCTTGTGTGTGTGATGACCCCGCAAGTTTGCACCTTTGAGCGCGCTGAGCT 598

Db 642 CGAAGTCTTGTGTGTGTGATGACCCCGCAAGTTTGCACCTTTGAGCGCGCTGAGCT 701

QY 599 CACGGCCCAAGTACTTGTGCGGAAGCTGTGATGATGACAGCCCTCGCGCTGC 658

Db 702 CACGGCCCAAGTACTTGTGCGGAAGCTGTGATGATGACAGCCCTCGCGCTGC 761

QY 659 CTGGCAGGCGCCAGTGACAGAGCCCTGACCTTTGCTTGAAGAAATAGCTGGGAG 718

Db 762 CTGGCAGGCGCCAGTGACAGAGCCCTGACCTTTGCTTGAAGAAATAGCTGGGAG 821

QY 719 GTGAAGTGGAGCGCTTCAGATGCTGATGATGATGATGATGATGATGATGATGATGAT 778

Db 822 GTGAAGTGGAGCGCTTCAGATGCTGATGATGATGATGATGATGATGATGATGATGAT 881

QY 779 GAGGAGGAGAGACACTCCGCGCAGATCTGCAAGTACTCTATTTCCGCGCAAGAGATC 838

Db 882 GAGGAGGAGAGACACTCCGCGCAGATCTGCAAGTACTCTATTTCCGCGCAAGAGATC 941

QY 839 CAAGAGCGCCCTCAGCGCTGCGCCCTGTGGGTGACCTCTTGTACCCCAAGTGAAGGAG 898

Db 942 CAAGAGCGCCCTCAGCGCTGCGCCCTGTGGGTGACCTCTTGTACCCCAAGTGAAGGAG 1001

QY 899 ACAGCAGCGAGCGCCCAAGTGTGCTGCGGTGTGATGATGATGATGATGATGATGATGAT 958

Db 1002 AAAGCAGCGAGCGCCCAAGTGTGCTGCGGTGTGATGATGATGATGATGATGATGATGAT 1059

QY 959 ATGAGTGT 966

Db 1060 ATGAGTGT 1067

RESULT 11

AL576710/c 972 bp mRNA linear EST 01-JUN-2003

LOCUS AL576710 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

DEFINITION clone CS0D1077YN05 3-PRIME, mRNA sequence.

ACCESSION AL576710

VERSION AL576710.2 GI:31314991

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 972)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT On Feb 16, 2001 this sequence version replaced gi:12939121.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by life technologies, a division of

OY		686	AGCTTTTGTCCGAAGAAGAAATGACTCTGGGAGGTGAACTGGACGCCTTACGATCGCT	745
Dd		951	AGCTTTCCTCRR-AAAAATGACTCTGGGAGGTGAACTGGGAGCSCTTMCAGATGCT	893
OY		746	GAACTACATTAACCTTCCTACGTATCTCGAGCGGGAGGAGGAGGACATCTCCGCCAGATC	805
Dd		892	GTACTACATAACTTCCTTACTTATTCTGCACGCGGGAGGAGGAGGACACTCTCCGCCAGATC	833
OY		806	CTGCAGAAATGACTCTTATTTGCCGCGCAGAAAGATCCAAAGAGCCCTGCACGCTCCGCCCTT	865
Dd		832	CTGCAGAAATGACTCTTATTTGCCGCGCAGAAAGATCCAAAGAGGCCCTGCACGCTCCGCCCTT	773
OY		866	GGGTGACTCTCTTGTAACCCCCAGGTGGGAAGCAGACAGCAGCAGCCCAATGCGTGGC	925
Dd		772	GGGTGACTCTCTTGTAACCCCCAGGTGGGAAGCAGACAGCAGCAGCCCAATGCGTGGC	713
OY		926	TGTAGTGTGACAGAGGCGCAGTGGGGCCCTGGAATGATGTGTGATGTGAGGCCCCTCCTGTG	985
Dd		712	TGTAGTGTGACAGAGGCGCAGTGGGGCCCTGGAATGATGTGTGATGTGAGGCCCCTCCTGTG	653
OY		986	CTGGGGGAATGAGCCACAGAACAGCAAGTAGCTTGCTCCCTGTGTCACCTAATGGGTG	1045
Dd		652	CTGGGGGAATGAGCCACAGAACAGCAAGTAGCTTGCTCCCTGTGTCACCTGAGGGTGG	593
OY		1046	TAGCAGAGTATGGCTCTCACCCCTCAGCCCTCAGTACTGTGGGCCCTTAATGGGCCAAGGCT	1105
Dd		592	TAGCAGAGTATGGCTCTCACCCCTCAGCCCTCAGTACTGTGGGCCCTTAATGGGCCAAGGCT	533
OY		1106	GCCCTGAGAACTGCTCCAGGCGCTGCACAGAGAGTGTGTGCAGACAGAAATGCTCCCAATT	1165
Dd		532	GCCCTGAGAACTGCTCCAGGCGCTGCACAGAGAGTGTGTGCAGACAGAAATGCTCCCAATT	473
OY		1166	TTTGTCTCAGAAATGAAAATTTTGGAGACCCTGCAAACAGAAAGGCTCATGTTTGCAGG	1225
Dd		472	TTTGTCTCAGAAATGAAAATTTTGGAGACCCTGCMAACAGCAAGGCTCATGTTTGCAGG	413
OY		1226	GGTGAGGCGCCCTCATCTATGAGGAAAGGTTTTGGATCTTGAAATGGGTCTCAGATATATC	1285
Dd		412	GGTGAGGCGCCCTCATCTATGAGGAAAGGTTTTGGATCTTGAAATGGGTCTCAGATATATC	353
OY		1286	TTATTCAGAGCTAAGGGTGGGTCTCAGAAATTAAGCAGGCAATTGAGGAAGACTCTTGCTT	1345
Dd		352	TTATTCAGAGCTAAGGGTGGGTCTCAGAAATTAAGGAGGCATTTGAGMAGAGCTTGCTT	293
OY		1346	CTCTCTACAGTGGCCAATCTCTCAACAACCCCTGAGGTCAAGGAGTGTGGCTCACAGTACA	1405
Dd		292	CTCTCTACAGTGGCCAATCTCTCAACAACCCCTGAGGTCAAGGAGTGTGGCTCACAGTACA	233
OY		1406	GCAATGTGCTTAATGCTTCATATGAGGAGATGTGCCCGGGCCAGAGGCTGTGTGAATGT	1465
Dd		232	GCAATGTGCTTAATGCTTCATATGAGGAGATGTGCCCGGGCCAGAGGCTGTGTGAATGT	173
OY		1466	GGGCACTGGCCAGAGTTCATACCTAATTTGCTA-----ATCAAAGCCAGGGTCTCTCCCT	1520
Dd		172	GGGCACTGGCCAGAGTTCATACCTAATTTGCTAATCTCACCTCACCCGCGGGGCTCTCCCT	113
OY		1521	CAGGTCTTTTAT--GAAGTCCGTGAATGTATGTATGTGTGTGGTCCCTCAGCTGAATGC	1579
Dd		112	CAGGTCTTTTATCGAAGTCCGTGAATGTATGTATGTGTGTGGTCCCTCAGCTGAATGC	53
OY		1580	CTCTGTGTGGGAAAGGGTGTGGGTGACAGTACATCATCAGGCTGTGGGC	1628
Dd		52	CTCTGTGTGGGAAAGGGTGTGGGTGAKNGKNCNTCATCAGGCTGTGGGC	4
<hr/>				
RESULT_13				
BX385986/c				
LOCUS BX385986 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA				
DEFINITION clone CS0DI025Yrb05 3-PRIME, mRNA sequence.				
ACCESSION BX385986				
VERSION BX385986.1 GI:30436712				


```
DB 553 GGGGAGGAGGCTGCTGAGAGAGCTCTCCAGGCTGCGACAGAGTGGTGGCAGACAGAG 494
QY 1155 TCTCCCTCAATTTTGTCTCAGAGTGAATAATCTTGGAGACCCCTGCAACAGACAGAGGTC 1214
DB 493 TCTCTCAATTTTGTCTCAGAGTGAATAATCTTGGAGACCCCTGCAACAGACAGAGGTC 434
QY 1215 ATGTTGCAAGGGGTAGAGGCGCCCTCATCTATGAGGAAGTTTGGATCTTGAATGTGTC 1274
DB 493 ATGTTGCAAGGGGTAGAGGCGCCCTCATCTATGAGGAAGTTTGGATCTTGAATGTGTC 374
QY 1275 TCAGGATATCTTATCAGAGCTAAGGGTGGGTGCTCAGATTAAGGACGAGCATTTGAGAG 1334
DB 373 TCAGGATATCTTATCAGAGCTAAGGGTGGGTGCTCAGATTAAGGACGAGCATTTGAGAG 314
QY 1335 AGCTTTGGTTCTCTCTACAGTGCACACTCTCAGACACCCCTGAGAGTCAAGGAGTGTG 1394
DB 313 AGCTTTGGTTCTCTCTACAGTGCACACTCTCAGACACCCCTGAGAGTCAAGGAGTGTG 254
QY 1395 CTCACAGTACAGATGTGCTTATGCTTATATAGAGAGATGTGCTGAGGCGCAGGTC 1454
DB 253 CTCACAGTACAGATGTGCTTATGCTTATATAGAGAGATGTGCTGAGGCGCAGGTC 194
QY 1455 TGTGGAATGTGGGACAGTGGCCAGGTCATACCTTATTTGCTATCAAGGACAGGTC 1514
DB 193 TGTGGAATGTGGGACAGTGGCCAGGTCATACCTTATTTGCTATCAAGGACAGGTC 134
QY 1515 CTCCTCAGTGTGTTTTATGAGAGTGCATGATGATGATGATGATGATGATGATGATGATG 1574
DB 133 CTCCTCAGTGTGTTTTATGAGAGTGCATGATGATGATGATGATGATGATGATGATGATG 74
QY 1575 AATGCTCTCTGTGGGGAAGGGGTGGGGTGCACATCA 1612
DB 73 AATGCTCTCTGTGGGGAAGGGGTGGGGTGCACATCA 36
```

```
RESULT 14
AL553818 1006 bp mRNA linear EST 31-MAY-2003
LOCUS AL553818 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
DEFINITION clone CSOD1077YN05 5-PRIME, mRNA sequence.
ACCESSION AL553818
VERSION AL553818.2 GI:31275632
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1006)
L1, W.B., Gruber, C., Jessup, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12894009.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2262.f for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CSOD1077G030P1c1cluster=2262.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1077G030P1.
Location/Qualifiers
1..1006
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1077YN05"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
```

FEATURES

```
source
1..1006
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1077YN05"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
```

```
BASE COUNT 222 a 278 c 313 g 189 t
ORIGIN
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
Query Match 52.8%; Score 886.8; DB 9; Length 1006;
Best Local Similarity 98.9%; Pred. No. 2.3e-143;
Matches 922; Conservative 2; Mismatches 4; Indels 4; Gaps 3;
QY 62 GGGGAGGGGAGAGGCGCTTCTTCAAAATGACCTTGAGACAGACAGACAGAGTGGTAC 121
DB 68 GGGGAGGGGAGAGGCGCTTCTTCAAAATGACCTTGAGACAGACAGACAGAGTGGTAC 127
QY 122 TGCAGCCAAAGAGACTCGGAGCTCGAGCTCGAGCTAGTACCTTACCGCGGAACCTGCTA 181
DB 128 TGCAGCCAAAGAGACTCGGAGCTCGAGCTCGAGCTAGTACCTTACCGCGGAACCTGCTA 187
QY 182 GCTGCAAGGCGCGCGGAGACAGAGAGCTGTGAGTGGAGACACCTGACCTTCT 241
DB 188 GCTGCAAGGCGCGCGGAGACAGAGAGCTGTGAGTGGAGACACCTGACCTTCT 247
QY 242 CAAGCTGAGTTGAGACAGAAATCAAGAGTACATGCCAGATCAACAGCAACTCTTC 301
DB 248 CAAGCTGAGTTGAGACAGAAATCAAGAGTACATGCCAGATCAACAGCAACTCTTC 307
QY 302 ATGAGCTTGAACAAGAGAGGTTCTTACAGAGCTTATCAAGGTTACAGTGAAGTGTG 361
DB 308 ATGAGCTTGAACAAGAGAGGTTCTTACAGAGCTTATCAAGGTTACAGTGAAGTGTG 367
QY 362 GCGCTGTCTGTGTCCTCCAGCAAGAGCAACCTCTTGCAGAGATGCCGGCGGAGC 421
DB 368 GCGCTGTCTGTGTCCTCCAGCAAGAGCAACCTCTTGCAGAGATGCCGGCGGAGC 427
QY 422 CCAGAGAGGGGACAAAGTGTACAGGCGCGCACTTCTTACCTGCCAAGATCTGTG 481
DB 428 CCAGAGAGGGGACAAAGTGTACAGGCGCGCACTTCTTACCTGCCAAGATCTGTG 487
QY 482 AAGCACTGTACATGCTGTCAAGCAAGAGGACGTGAAGTATGAGAGCCCTGTGGA 541
DB 488 AAGCACTGTACATGCTGTCAAGCAAGAGGACGTGAAGTATGAGAGCCCTGTGGA 547
QY 542 AAGTCTTGTGTGTGATGATGACCCCGCAAGTTTGCATCTTTGACGCGGTGAGCTAC 601
DB 548 AAGTCTTGTGTGTGATGATGACCCCGCAAGTTTGCATCTTTGACGCGGTGAGCTAC 607
QY 602 GGGCAAGGTACTTGGAGAGCTGTGATGATGAGAGCCCGGCGGCTGGCTCTG 661
DB 608 GGGCAAGGTACTTGGAGAGCTGTGATGATGAGAGCCCGGCGGCTGGCTCTG 667
QY 662 GCAGGCGCCAGTGAAGAGCCCTGAGCTTGTCTGGAAGGAATAATGACTGTGGAGGTG 721
DB 668 GCAGGCGCCAGTGAAGAGCCCTGAGCTTGTGTCTGGAAGGAATAATGACTGTGGAGGTG 727
QY 722 AACTGGAGCGCTTACAGATGCTGTAATCAATTAATCTTACATCTGACGAGGAG 781
DB 728 AACTGGAGCG-CTTACAGATGCTGTAATCAATTAATCTTACATCTGACGAGGAG 786
QY 782 GAGGAGGAGCACTCCGCAAGTCTGCAAGAGTACCTTGTGGCGGCAAGATCCAA 841
DB 787 GAGGAGGAGCACTCCGCAAGTCTGCAAGAGTACCTTGTGGCGGCAAGATCCAA 846
QY 842 GAGGCGCTGACAGCTGCGCCCTTGGTGGTACCTTGTGAACCCCAAGTGAAGCAGACA 901
DB 847 GAGGCGCTGACAGCTGCGCCCTTGGTGGTACCTTGTGAACCCCAAGTGAAGCAGACA 906
QY 902 GCAGGACAGCCAAAGTGTGCTGCTGTGATGTGACAGGCGCACTGTGGGCTGTGGAATG 961
DB 907 GCAGGACAGCCAAAGTGTGCTGCTGTGATGTGACAGGCG-AGTGGGCTGTGGAATG 964
QY 962 AGTGTGATGAGAGCCCTCTGTGTGGGGA 993
```


Db	133	CTGACACCCCTTGGCCCTCATTTACTGAGGCGCTTAGTGAGCCCAAGGGCTGCCTTAGAAGCTGC	192
OY	1121	TCGAGGCCCTGACGAGGAGGTGGTGCAGACACAAGCTCTCGAAATTTTGTGTCAGAACTG	1180
Db	193	TCGAGGCCCTGACGAGGAGGTGGTGCAGACACAAGCTCTCGAAATTTTGTGTCAGAAAGTGG	252
OY	1181	AAAAATCTTGGAGACCCCTGCAGAACAGAACAGGGTCATGTTTGCAGGGGTAGAGGCCCTCAT	1240
Db	253	AAAAATCTTGGAGAACCCCTGCAGAACAGAACAGGGTCATGTTTGCAGGGGTAGAGGCCCTCAT	312
OY	1241	CTTAGAGAGAAAGTTTGGATCTTGAATGTGGTCTCAGAGTAATCCTTATCAGAGCTTAGG	1300
Db	313	CTATGAGAGAAAGGTTTGGATCTTGAATGTGGTCTCAGAGTAATCCTTATCAGAGCTTAGG	372
OY	1301	GTGGGTGCTCAGAAATPAGGCAGGCA-TTGAAGAAAGTCTTGGTTCCTCTACAGTGGC	1359
Db	373	GTGGGTGCTCAGAAATPAGGCAGGCAATTTGANGAAAAAATCTTGGGTTCCTCTTACAGTGGC	432
OY	1360	AACCTCTACACACCCCTGAGGTTCAGGGGAGTCTGGCTCACA 1400	
Db	433	CACCTTCTACACACCCCTTGAAGGCAAGAAATCTTGGCTTACA 473	

```

RESULT 2
US-09-614-069-2
: Sequence 2, Application US/09614069
: Patent No. 6485910
GENERAL INFORMATION:
APPLICANT: Walker, Michael G.
APPLICANT: Klingner, Tod M.
APPLICANT: Kresnow, Randi E.
TITLE OF INVENTION: RAS ASSOCIATION DOMAIN CONTAINING PROTEIN
FILE REFERENCE: PC-0014 CIP
CURRENT APPLICATION NUMBER: US/09/614,069
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 09/023,655
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 09/195,292
PRIOR FILING DATE: 1998-11-18
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PERL Program
SEQ ID NO 2
: LENGTH: 3144
: TYPE: DNA
: ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
: OTHER INFORMATION: incyte ID No: 6485910 2726173CH1
US-09-614-069-2

```

Query Match	14.1%;	Score 236.8;	DB 4;	Length 3144;
Best Local Similarity	60.6%;	Pred. No. 4.6e-58;		
Matches 388; Conservative	0;	Mismatches 252;	Indels 0;	Gaps 0;

[illegible][illegible]

RESULT 3
US-08-942-572-1
; Sequence 1, Application US/08942572
; Patent No. 6140488

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

```

1  ATTORNEY/AGENT INFORMATION:
2  NAME: Fraser, Janis K.
3  REGISTRATION NUMBER: 34,819
4  REFERENCE/DOCKET NUMBER: 064472/737001
5  TELECOMMUNICATION INFORMATION:
6  TELEPHONE: 617/542-5070
7  TELEFAX: 617/542-8906
8  TELEX: 200154
9  INFORMATION FOR SEO ID NO: 1:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 3018 base pairs
12 TYPE: nucleic acid
13 STRANDEDNESS: single
14 TOPOLOGY: linear
15 MOLECULE TYPE: cDNA
16 FEATURE:
17 NAME/KEY: Coding Sequence
18 LOCATION: 31...1269
19 OS-08-942-572-1

```

Query Match 13.2%; Score 221.2; DB 3; Length 3018;
 Best Local Similarity 57.5%; Pred. No. 1.4e-53;
 Matches 397; Conservative 0; Mismatches 293; Indels 0; Gaps 0;

```

OY 171 GAACTCGCTAGCTGGCAGGCGCCGCGGACACAGCAGCCTTGAGTGGAGACAC 230
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 566 GAAAGACCTTCACCCCAACCTTGAACCAAGATGTGTGAAGCACTGAGGAGACACAC 625
OY 231 CTGACCTTCTCAAGCTGAGATTGAGCAGAAATGATCAAGAGTACATGCCAGATCAACA 290
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 626 ACCGCCCAACGATACAGAGATCAAGCAGAGATTTGACGCTATTAACAGCAGGAGAAC 685
OY 291 GCACCTCTTCTGAGCTTGAACAAGAGAGGTTCTTACACAGCCTTCATCAAGGTTGACG 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 686 ACTGCTGGGATGAAAGCTGAGTAAGATGGCACTACACAGGTTTCATCAAGATGACAT 745
OY 351 TGAACCTGCTGCGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 410
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 746 TGAACCTGCGAGCGGCTGAGAGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCTGCTG 805
OY 411 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 806 CCATTAGAGAACTGAACCTCTGACGACGACGACGACGACGACGACGACGACGACGAC 865
OY 471 AGGATGCTGTCAAGCACTGATGCTGTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 530
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 866 TCGATGCTCATCAAGCAAGCTATCAATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 925
OY 531 CCGCTCTGGAAGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 590
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 926 GCGCTCTCAAGAACTGATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 985
OY 591 CTGACGCTCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 986 TACACAAAGATGACAGAGTCTTCCAGAACTCTCCATCTCTGATCTCTCTCTAC 1045
OY 651 TCGGCTCTCTGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 710
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1046 TTGCTCTGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1105
OY 711 CTGGGGAGGTGAACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 770
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1106 CTGGAGAGGTGAGTGGGATGCTTTCATCTCTGAACTCCAGAACTTTTAACTATCC 1165
OY 771 TGCACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 830
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1166 TGGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1225
OY 831 AGAAGATCCAGAGGCGGCTGACGCGCTGCC 860
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1226 AGAAACTGGAAGAGGAGATTAAGAGAGTCC 1255
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 4
 US-09-484-970B-23
 ; Sequence 23, Application US/09484970B
 ; Patent No. 6426186

GENERAL INFORMATION:
 APPLICANT: Jones, Karen A.
 APPLICANT: Volkmutch, Wayne
 TITLE OF INVENTION: BONE REMODELING GENES
 FILE REFERENCE: PB-0014 US
 CURRENT APPLICATION NUMBER: US/09/484,970B
 CURRENT FILING DATE: 2000-01-18
 NUMBER OF SEQ ID NOS: 172
 SOFTWARE: PERL Program
 SEQ ID NO 23

LENGTH: 3030
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:

NAME/KEY: misc_feature
 OTHER INFORMATION: Incyte ID No. 6426186 218628.2CB1
 NAME/KEY: unsure
 LOCATION: 9, 64
 OTHER INFORMATION: a, t, c, g, or other
 US-09-484-970B-23

Query Match 7.8%; Score 131; DB 4; Length 3030;
 Best Local Similarity 60.1%; Pred. No. 1.4e-27;
 Matches 218; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

```

OY 248 GAGATTGACCAAGATCAAGAGTACAAATGCCAGATCAAGCAACCTCTTCAATGAC 307
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 211 GAGATCAACAGAAATGATCAGAGCTTCAACACGCGAGAGAAATGCTGGGATGAAA 270
OY 308 TTGAACAAGAGGTTCTTCAACAGGCTTCAACAGGTTGACCTGAGAGTGGTGGCCCT 367
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 271 CTGAGTGAAGAGGCGCACTTACAGGTTTCAAAAGTCAATCTGAACTCCGGGCGCT 330
OY 368 GTCTGTGCTCTCCAGCAAGAACCCCTCTTCAAGATGCGCGGCGGCGGCGGCGGCGG 427
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 331 GTAGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 390
OY 428 CCGGCGCAAGTGTCAAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 487
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 391 CTGGCGGCTACCAAGGAGCAAGGAGATCTTCTTACCTGCTGATGATCAAGCAG 450
OY 488 CTGCATGCTCTGCTACAGCAAGGAGGAGCAAGTATGAGGCTGCTGCGAAAGTTTC 547
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 451 CTGCACATACAGACACCAACCGTCACTGAGTATCCAGGGGCTGCTCAAGAAATTC 510
OY 548 TTGTGTGTGAGAGACCCCGCAAGTTTGCACTCTTGTGAGCGGCTGAGCGTACGCGCAA 607
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 511 ATGGTGTGTGACAAATCCCAAGATTGCACTTTTAAACGGATTAACAAGAGCGAGCAA 570
OY 608 GTG 610
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 571 GTG 573
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 5
 US-09-614-069-4
 ; Sequence 4, Application US/09614069
 ; Patent No. 6485910

GENERAL INFORMATION:
 APPLICANT: Walker, Michael G.
 APPLICANT: Klingler, Tod M.
 TITLE OF INVENTION: RAS ASSOCIATION DOMAIN CONTAINING PROTEIN
 FILE REFERENCE: PC-0014 CIP
 CURRENT APPLICATION NUMBER: US/09/614,069
 CURRENT FILING DATE: 2000-07-11
 PRIOR APPLICATION NUMBER: 09/023,655
 PRIOR FILING DATE: 1998-02-09
 PRIOR APPLICATION NUMBER: 09/195,292
 PRIOR FILING DATE: 1998-11-18
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PERL Program
 SEQ ID NO 4
 LENGTH: 510
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: Incyte ID No. 6485910 2726173P6
 NAME/KEY: unsure
 LOCATION: 338, 498, 502, 506
 OTHER INFORMATION: a, t, c, g, or other
 US-09-614-069-4

Query Match 3.7%; Score 62.4; DB 4; Length 510;
 Best Local Similarity 66.2%; Pred. No. 3.1e-08;
 Matches 90; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

RESULT 11
US-09-252-991A-13757
; Sequence 13757, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/094,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13757
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13757

Query Match 2.2%: Score 37.8; DB 4; Length 1119;
Best Local Similarity 50.3%; Pred. No. 0.59;
Matches 93; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 552 TGTGATGACCCCGCAAGTTTGACTTTGAGCCGCTGACGCTCAGCCCAAGTGT 611
DB 455 TGGCGGGCGCCCGCAGCGAGAGACCTCAGCTGCGGCGCTATGTGACAGCGTGTG 514
QY 612 ACTGCGGAAGCTTTGATATAGACAGCCCCCTGCGGCTCGCTCTGCGAGGCCCA 671
DB 515 CTTGAGGAGCGGCTGCGCCGCGACCCGCTTCTCCCGCTATCTGCTGCGCATYA 574
QY 672 GTGACAAGGCGCTGCTTGTCTGGAAGAAATGACTGTGGGAGAGTAAGTGGACG 731
DB 575 GCGAAGCGCGCTATGCTCCAGCCTGGGCGGCGCTCGACCGCGCGGAGAAATTGATCG 634
QY 732 CCTTC 736
DB 635 CCATC 639

RESULT 12
US-09-252-991A-13376/c
; Sequence 13376, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/094,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13376
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13376

Query Match 2.2%: Score 37.8; DB 4; Length 1389;
Best Local Similarity 50.3%; Pred. No. 0.66;
Matches 93; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 552 TGTGATGACCCCGCAAGTTTGACTTTGAGCGGCTGACGCTCAGCCCAAGTGT 611
DB 1049 TGGCGGGCGCCCGCAGCGAGAGACCTCAGCTGCGGCGCTATGTGACAGCGTGTG 990

QY 612 ACTGCGGAAGCTTTGATATAGACAGCCCCCTGCGGCTCGCTCTGCGAGGCCCA 671
DB 989 CTTGAGGAGCGGCTGCGCCCGCAGCCCGCTTCTCCCGCTATCTGCTGCGGCATA 930
QY 672 GTGACAAGGCGCTGATGCTTGTCTGGAAGAAATGACTGTGGGAGAGTAAGTGGACG 731
DB 929 GCGAAGCGCGCTATGCTCCAGCCTGGGCGGCTCGACCGCCGCGGAGAAATTGATCG 870
QY 732 CCTTC 736
DB 869 CCATC 865

RESULT 13
US-09-252-991A-4618/c
; Sequence 4618, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/094,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4618
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4618

Query Match 2.2%: Score 37.4; DB 4; Length 402;
Best Local Similarity 50.9%; Pred. No. 0.44;
Matches 89; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 1 CCGGGCGGCTGTGCGGCTACGACGCGGAGACTGGGGAGCGGGTACGGCTAT 60
DB 252 CAGCAGCGCTGATGATGAGTGTGATGCTCCCGCGCTGATGGGGCGATCGCGGC 193
QY 61 GCGGAGGCGGAGCGCCCTTCTTTCGAATGACCTGAGCAGCAGCAGCAGTGGCTA 120
DB 192 GCTGTCCGCGAGCTGTGCTTCACGCGCTGAGCTGGCGGCGCGGAGCAACTCTCTG 133
QY 121 CTGAGCCAGAGACTGCGACTGCGAGCTGAGCTGAGCTTACCCGCGCAACC 175
DB 132 GCGTGGCGCGGAGCTGCGCAATGCCATCGGGGACTGCGCCAGCAGAGAGGCC 78

RESULT 14
US-09-252-991A-9804
; Sequence 9804, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/094,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9804
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9804

Query Match 2.2%; Score 37.4; DB 4; Length 744;
Best Local Similarity 50.3%; Pred. No. 0.62;
Matches 92; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Search completed: August 20, 2003, 09:54:34
Job time : 117.3 secs

OY 561 ACCCCGCAAGTTTGACCTCTTGAGCGGCTGAGCGCCCAAGTACTTCCGGA 620
DB 470 ATCACCCTCGCTCGCTCGACAGCGGATGAGATCCACCAAGGCTCTGCGCG 529
OY 621 ACCTGTGATGATGAGCAGCCCTGCGGCTGCTGCGAGGCGCCAGTGACAAG 680
DB 530 TGGTATGAGACCTCTCGCTCCCTCTCTGACGACTGGCGCGAGCCAGTGATGAG 589
OY 681 CCTGAGCTTCTCTGAAGAAATGACTGTGGGAGGTGAATGGACGCTTCAGCA 740
DB 590 TCCTCACCCAGCAGATGTGACCGCCCTGCGAGGAGAGATCGGCAACGTCTGCGCT 649
OY 741 TGC 743
DB 650 GGC 652

RESULT 15

US-09-461-325-471
; Sequence 471, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; EARLIER FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 471
; LENGTH: 1221
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-325-471

Query Match 2.2%; Score 37.4; DB 4; Length 1221;
Best Local Similarity 48.8%; Pred. No. 0.8;
Matches 101; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

OY 593 GAGCGTCACGCGCACTGCTGCGGAGCTGTGGATGAGACGCCCTGCGGCTG 652
DB 802 GACCCGACACGCGCGCTGCGCTGCGAGCTGGAGTGGCAACCGGATGTGCTG 861
OY 653 CGGCTCCTGCGAGCGCCAGTGACAAAGCGCTGAGCTTGTCTGGAAGAAATGACTCT 712
DB 862 CAGTTCTCGCTGCTGCTGCTGCGAGGAGACAGCGCTTATAGCTGACCTGACCC 921
OY 713 GGGAGGTGACTGGAGCGCTTCAAGATGCTGAATCAATTAATTAATTAATTA 772
DB 922 GTGGCGGCGCAGCTGGGCGCCACACCGCCAGCGGCGCTTCCGTACCCCTTCTCC 981
OY 773 CAGCGGAGAGAGAGAGACCTCCGC 799
DB 982 ACTGGGACACGAGATCAGACCTCCGC 1008

THIS PAGE BLANK (USPTO)

QY 121 CTGACCCAGAGAGACTCGAGCTCGAGAGCTGAGAGTACTTTCACCCGGGCAACCTGCT 180
 Db 121 CTGACCCAGAGAGACTCGAGCTCGAGAGCTGAGAGTACTTTCACCCGGGCAACCTGCT 180
 QY 181 AGCTGCGAGCGCGCGCGGACCAAGAGAGCTGAGAGTACTTTCACCCGGGCAACCTGCT 240
 Db 181 AGCTGCGAGCGCGCGCGGACCAAGAGAGCTGAGAGTACTTTCACCCGGGCAACCTGCT 240
 QY 241 TCAAGCTGAGATGAGAGAGATCAAGAGATCAAGAGATCAAGAGATCAAGAGATCAAG 300
 Db 241 TCAAGCTGAGATGAGAGAGATCAAGAGATCAAGAGATCAAGAGATCAAGAGATCAAG 300
 QY 301 CATAGAGTGAACAAGAGAGCTTCTTACAGAGCTTCTTACAGAGCTTCTTACAGAGCT 360
 Db 301 CATAGAGTGAACAAGAGAGCTTCTTACAGAGCTTCTTACAGAGCTTCTTACAGAGCT 360
 QY 361 GCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 Db 361 GCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 421 CCCAGAGAGCGGCGCAAGAGTGTACAGCGCGCGCTTCTTACAGAGCTTCTTACAGAGCT 480
 Db 421 CCCAGAGAGCGGCGCAAGAGTGTACAGCGCGCGCTTCTTACAGAGCTTCTTACAGAGCT 480
 QY 481 CAACACCTGATGATGCTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 Db 481 CAACACCTGATGATGCTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 541 AAAGTCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
 Db 541 AAAGTCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
 QY 601 CGGCCAAGGTACTTGGGGAAGCTGTGGATGATGAGAGAGAGAGAGAGAGAGAGAGAG 660
 Db 601 CGGCCAAGGTACTTGGGGAAGCTGTGGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 QY 661 GGGGAGGCGCGAGTACAAAG 720
 Db 661 GGGGAGGCGCGAGTACAAAG 720
 QY 721 GAAGTGGAG 780
 Db 721 GAAGTGGAG 780
 QY 781 GAG 840
 Db 781 GAG 840
 QY 841 AG 900
 Db 841 AG 900
 QY 901 AG 960
 Db 901 AG 960
 QY 961 GAGTGTGATGAG 1020
 Db 961 GAGTGTGATGAG 1020
 QY 1021 TGCTCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 Db 1021 TGCTCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 QY 1081 TACTGAGGCTTACTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
 Db 1081 TACTGAGGCTTACTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
 QY 1141 GGTGACACAG 1200
 Db 1141 GGTGACACAG 1200
 QY 1201 AACGAGACAG 1260

Db 1201 AACGAGACAG 1260
 QY 1261 TCTTGAATGAG 1320
 Db 1261 TCTTGAATGAG 1320
 QY 1321 AGGATGAG 1380
 Db 1321 AGGATGAG 1380
 QY 1381 TCAG 1440
 Db 1381 TCAG 1440
 QY 1441 CCTGGGAG 1500
 Db 1441 CCTGGGAG 1500
 QY 1501 CAAAGCCAG 1560
 Db 1501 CAAAGCCAG 1560
 QY 1561 GGTGGCTCAG 1620
 Db 1561 GGTGGCTCAG 1620
 QY 1621 CCTGGGAG 1680
 Db 1621 CCTGGGAG 1680
 RESULT 2
 US-09-821-803A-5
 : Sequence 5, Application US/09821803A
 : Patent No. US20020098530A1
 : GENERAL INFORMATION:
 : APPLICANT: Pfeiffer, Gerd P.
 : TITLE OF INVENTION: Lung Cancer Tumor Suppressor Gene
 : FILE REFERENCE: 1954-335-II
 : CURRENT APPLICATION NUMBER: US/09/821,803A
 : PRIOR FILING DATE: 2001-03-30
 : PRIOR FILING DATE: 2000-03-30
 : NUMBER OF SEQ ID NOS: 19
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 5
 : LENGTH: 1692
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (12)..(821)
 : US-09-821-803A-5
 Query Match 95.4%; Score 1602.6; DB 9; Length 1692;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1628; Conservative 0; Mismatches 4; Indels 3; Gaps 2;
 QY 48 CGGCTAGGAG 107
 Db 1 CGGCTAGGAG 60
 QY 108 CGAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 167
 Db 61 CGAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 QY 168 CGGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 227
 Db 121 CGGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 QY 228 CAGCTGACCTTCTCAAGCTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCA 287

OY	730	GGCTTCAGCAATGGCTGAACATCAATCAATCTCTACATCTCGACGGGGAGGAGAGGA	789
Db	710	GGCTTCAGCAATGGCTGAACATCAATCTCTACATCTCGACGGGGAGGAGAGGA	769
OY	790	GCACCTCCGCGACATCTCTGACAGAACTACTCTATATGGCCGCGACAGAAATCCAAAGGCGCT	849
Db	770	GCACCTCCGCGACATCTCTGACAGAAATCTCTATATGGCCGCGACAGAAATCCAAAGGCGCT	829
OY	850	GCACGCTGCCCTTGGGTGACCTCTTTGATACCCCGACAGTGGAAAGGACAGACAGAGCAG	909
Db	830	GCACGCTGCCCTTGGGTGACCTCTTTGATACCCCGACAGTGGAAAGGACAGACAGAGCAG	889
OY	910	CGCCAAAGCGGTGGCGGTGTGATGTGACAGGGGCGAGTGGGGCCGTGGAAATGAGTGTGCA	969
Db	890	CGCCAAAGCGGTGGCGGTGTGATGTGACAGGGGCGAGTGGGGCCGTGGAAATGAGTGTGCA	949
OY	970	TGAGAGCCCTTCCTTCGTGTGGGGGAATGAGCCACAGAACAGCAAGTACGTTCCTCTG	1029
Db	950	TGAGAGCCCTTCCTTCGTGTGGGGGAATGAGCCACAGAACAGCAAGTACGTTCCTCTG	1009
OY	1030	TGTCCACCTATGGGTGTAGCCAGGTATGGCTCTGCACCCCTCTGCGCTCATTTACTGGGCC	1089
Db	1010	TGTCCACCTATGGGTGTAGCCAGGTATGGCTCTGCACCCCTCTGCGCTCATTTACTGGGCC	1069
OY	1090	TTAGTGGGCCAGGGCTGCCCTGAGAAAGTGTGTCCAGGCTGACAGAGAGTGGTGCACAC	1149
Db	1070	TTAGTGGGCCAGGGCTGCCCTGAGAAAGTGTGTCCAGGCTGACAGAGAGTGGTGCACAC	1129
OY	1150	AGAACTCTCCCAATTTTTGTCTCAGAAATGAAATCTTGGAGACCTCGCAACAGAAACA	1209
Db	1130	AGAACTCTCCCAATTTTTGTCTCAGAAATGAAATCTTGGAGACCTCGCAACAGAAACA	1189
OY	1210	GGGTCAATGTTTGCAGGGGTGACGGCCCTCATCTATGAGAAAGTTTTGATCTTGAATG	1268
Db	1190	GGGTCAATGTTTGCAGGGGTGACGGCCCTCATCTATGAGAAAGTTTTGATCTTGAATG	1249
OY	1270	TGGTCTAGAGATACCTTATACAGAGCTTAAGGGGTGGGTCTCAGAAATGAGGACGATGGA	1329
Db	1250	TGGTCTAGAGATACCTTATACAGAGCTTAAGGGGTGGGTCTCAGAAATGAGGACGATGGA	1309
OY	1330	GGAAAGATCTTGTGTTTCTCTACAGTGCACAACTCTCACACACCCTGAGGTGCAGGAGT	1389
Db	1310	GGAAAGATCTTGTGTTTCTCTACAGTGCACAACTCTCACACACCCTGAGGTGCAGGAGT	1369
OY	1390	GCTGGCTCACAGTACAGCATGTGCCCTTAATCTTCATATGAGAGAGATGTCCCTGGGCCA	1449
Db	1370	GCTGGCTCACAGTACAGCATGTGCCCTTAATCTTCATATGAGAGAGATGTCCCTGGGCCA	1429
OY	1450	GGGTCTGTGTAAATGTGGGCACTGGGCCAGGTTCAATACCTTATTTGCTAATCAAAGCCAG	1509
Db	1430	GGGTCTGTGTAAATGTGGGCACTGGGCCAGGTTCAATACCTTATTTGCTAATCAAAGCCAG	1489
OY	1510	GGTCTCTCCCTCAGAGTG-TTTTATGAAAGGCGTGAATGTATGTAATGTGTGGGCGCT	1568
Db	1490	GGTCTCTCCCTCAGAGTGTTTATGAAAGTGCCTGAATGTATGTAATGTGTGGGCGCT	1549
OY	1569	CAGCTGAATGCTCTCTGTGGGAAAGGGGTTGGGGTGCACAGTCAATCAAG--CTTGGG	1626
Db	1550	CAGCTGAATGCTCTCTGTGGGAAAGGGGTTGGGGTGCACAGTCAATCAAGCGCTGGGG	1609
OY	1627	GCTAAGAAATTTGGCTCAATTAATATTTCAAGATTCGCAAAAAAAAAAAAAAAAAAAAA	1680
Db	1610	CCTAAGAAATTTGGCTCAATTAATATTTCAAGATTCGCAAAAAAAAAAAAAAAAAAAAA	1663

RESULT 5
US-09-796-692-5016/c

```

; Sequence 5016, Application US/09796692
; Publication No. US20020198362A1
;
; GENERAL INFORMATION:
; APPLICANT: Galger, Alexander
; APPLICANT: Algate, Paul A.

```

```

APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5016
LENGTH: 432
TYPE: DNA
ORGANISM: Homo sapiens
US-09-796-692-5016

```

Query Match	25.7%	Score 432	DB 10	Length 432
Best Local Similarity	100.0%	Prod. No.	2,6e-125	
Matches 432	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1140	TGtGtCAGACAGAAgTcTcTCAATTTTTTgTcTcAGAAgTGAATCTTgGAGACCCtGc	1195	
Db	432	TGgTgCAGACAGAAgTcTcTCAATTTTTTgTcTcAGAAgTGAATCTTgGAGACCCtGc	373	
QY	1200	AAACAGAAcAGGgTcATgTTTgCAGGGGTgAGGGCCcCArCTATgAGAAAGgTTTgG	1255	
Db	372	AAACAGAAcAGGgTcATgTTTgCAGGGGTgAGGGCCcCArCTATgAGAAAGgTTTgG	313	
QY	1260	ATcTTGAATgTgTcTcTcAGATATcCTATcAGAGCTAAAGGTGGGTcTcTcAGAAATAgG	1319	
Db	312	ATcTTGAATgTgTcTcTcAGATATcCTATcAGAGCTAAAGGTGGGTcTcTcAGAAATAgG	253	
QY	1320	CAGGCATTTGAAGAAAGATcTtGgTTTcTcTcTACAGTcGCAATcCTcTACACACCCtAg	1379	
Db	252	CAGGCATTTGAAGAAAGATcTtGgTTTcTcTcTACAGTcGCAATcCTcTACACACCCtAg	193	
QY	1380	GTCAGGGAGTgTcTcTcGCTcACAGTcACAGCATgTGCCTTAATcCTcATATGAAGAGATG	1438	
Db	192	GTCAGGGAGTgTcTcTcGCTcACAGTcACAGCATgTGCCTTAATcCTcATATGAAGAGATG	133	
QY	1440	CCCTGGGGCAGAGTcTcTgTGAATgTGGGCACTGGCCAGTTCArTACCTTAATTTGCTAA	1499	
Db	132	CCCTGGGGCAGAGTcTcTgTGAATgTGGGCACTGGCCAGTTCArTACCTTAATTTGCTAA	73	
QY	1500	TCAAAGCAGAGGTcTcTcCCCTcCAGGTgTTTTTAATGAAGTcCGTAATGTATGTAAATG	1558	
Db	72	TCAAAGCAGAGGTcTcTcCCCTcCAGGTgTTTTTAATGAAGTcCGTAATGTATGTAAATG	13	
QY	1560	TGtGtGcCCTcAG 1571		
Db	12	TGtGtGcCCTcAG 1		

Db 253 AAAATCTTGGAAACCTGCAACAGACAGAGGCTCATGTTTTCAGGGGTGACGGCCCTCAT 312
Qy 1241 CATATGAGAAAGATTTTGGATCTTGAATGTGCTCAGAGATATCCTTATCAGAGCTAAG 1300
Db 313 CATATGAGAAAGATTTTGGATCTTGAATGTGCTCAGAGATATCCTTATCAGAGCTAAG 372
Qy 1301 GTGGGTGCTCAGAAATAGGACGCA-TTGAGAGAGAGTCTTGCTTCTCTACAGTGGC 1359
Db 373 GTGGGTGCTCAGAAATAGGACGCAATTTGANGAAAAATCTTGAGTCTCTTACAGTGGC 432
Qy 1360 AACTCTGACACACCTGAGGAGTGGTGGCTGCA 1400
Db 433 CACTTCTTACACACCTTGAGGCAAGAAATGCTGCTTACA 473

RESULT 8
US-09-796-692-3636/c
Sequence 3636, Application US/09796692
Publication No. US20020198362A1
GENERAL INFORMATION:
APPLICANT: Galiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3636
LENGTH: 446
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (409)
OTHER INFORMATION: n-A,T,C or G
US-09-796-692-3636

Query Match 24.0%; Score 402.6; DB 10; Length 446;
Best Local Similarity 97.6%; Pred. No. 4,7e-116;
Matches 408; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 709 CTCGTGGAGAGTGAATGAGGAGCGCTTTCAGATGCTGAACTACATACCTCTAGCTAT 768
Db 418 CTTTGGCCNTGTCAGTGGAGCGCTTTCAGATGCTGAACTACATACCTCTAGCTAT 359
Qy 769 CCTGACGGGAGAGAGGAGACACCTCCGACAGATCTGCAAGAACTACTCTATTGCGG 828

Db 358 CCTGACGGGAGAGAGAGACACCTCCGACAGATCTGCAAGAACTACTCTATTGCGG 299
Qy 829 CCAGAAATCCAAAGAGGCCCTGACAGCCCTGCCCCCTGGGTGATACCTCTGTCACCCAG 888
Db 298 CCAGAAATCCAAAGAGGCCCTGACAGCCCTGCCCCCTGGGTGATACCTCTGTCACCCAG 239
Qy 889 TGAAGGACAGACAGCAGGAGCGCCAAAGTGCCTGCGTGTGATGTGACAGGGCCAGTGG 948
Db 238 TGAAGGACAGACAGCAGGAGCGCCAAAGTGCCTGCGTGTGATGTGACAGGGCCAGTGG 179
Qy 949 GGCCTGTGGAATGATGTGCAATGAGAGCCCTCTGCTGTGGGGGAATGAGCCAGAGAAC 1008
Db 178 GGCCTGTGGAATGATGTGCAATGAGAGCCCTCTGCTGTGGGGGAATGAGCCAGAGAAC 119
Qy 1009 AGCGAATGATGCTGCTCCCTGTGTCCACCTATGGGTGATGCGCAGATGAGCTGTACACC 1068
Db 118 AGCGAATGATGCTGCTCCCTGTGTCCACCTATGGGTGATGCGCAGATGAGCTGTGTACACC 59
Qy 1069 CTCGTGCCCTCATTTACTGGGCTTATGAGGCGCAGAGGCTGCGCTGAGAACTGCTCAGG 1126
Db 58 CTCGTGCCCTCATTTACTGGGCTTATGAGGCGCAGAGGCTGCGCTGAGAACTGCTCAGG 1

RESULT 9
US-10-040-862-3636/c
Sequence 3636, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Galiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retler, Marc
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther
FILE REFERENCE: 014058-01352005
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3636
LENGTH: 446
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure

LOCATION: (409)
OTHER INFORMATION: n-A,T,C or G
US-10-040-862-3636

Query Match 24.08; Score 402.6; DB 14; Length 446;
Best Local Similarity 97.6%; Pred. No. 4,7e-116;
Matches 408; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 709 CTCTGGGAGGTGAAGTGGGAGCGGCTTGCAGCATCCCTGAAGTACATTAATCTTCCACGAT 768
DB 418 CTTTGGCCCTMTTGCAGTGGGAGCGGCTTGCAGCATCCCTGAAGTACATTAATCTTCCACGAT 359
QY 769 CCTTCAGCGGAG 828
DB 358 CCTTCAGCGGAG 299
QY 829 CCAGAAATCCAAAG 888
DB 298 CCAGAAATCCAAAG 239
QY 889 TGAAGGAG 948
DB 238 TGAAGGAG 179
QY 949 GGCTGTGGAATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1008
DB 178 GGCTGTGGAATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 119
QY 1009 AGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1068
DB 118 AGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 59
QY 1069 CTCTGCCCTCAATTAAGTGGGAG 1126
DB 58 CTCTGCCCTCAATTAAGTGGGAG 1

RESULT 10

US-09-803-719-1629
Sequence 1629, Application US/09803719
Publication No. US20030044783A1
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Escobedo, Jaime
APPLICANT: Immls, Michael A.
APPLICANT: Garcia, Pablo Dominguez
APPLICANT: Sudduth-Klinger, Julie
APPLICANT: Reinhard, Christoph
APPLICANT: Gliese, Klaus
APPLICANT: Randerzo, Filippo
APPLICANT: Kennedy, Giulia C.
APPLICANT: Pot, David
APPLICANT: Kassam, Altaf
APPLICANT: Lamson, George
APPLICANT: Drmanac, Radjoje
APPLICANT: Crtvenjakov, Radomir
APPLICANT: Dickson, Mark
APPLICANT: Drmanac, Snezana
APPLICANT: Labat, Ivan
APPLICANT: Leshkowitz, Dena
APPLICANT: Kila, David
APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Human Genes and Gene Products
FILE REFERENCE: 1624. 002
CURRENT APPLICATION NUMBER: US/09/803,719
CURRENT FILING DATE: 2001-03-09
PRIORITY APPLICATION NUMBER: 60/188,609
PRIORITY FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 2396
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1629

LENGTH: 381
TYPE: DNA
ORGANISM: Homo sapiens
US-09-803-719-1629

Query Match 22.08; Score 368.8; DB 11; Length 381;
Best Local Similarity 99.5%; Pred. No. 1.9e-105;
Matches 370; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 848 CTGCAGCCCTGACCTTGGGTGACCTTGTGACCCCGAGGTGAGAGAGAGAGAGAGAGAGAGAG 907
DB 10 CGGCAGCCCTGACCTTGGGTGACCTTGTGACCCCGAGGTGAGAGAGAGAGAGAGAGAGAGAG 69
QY 908 AGCCCAAGTGCCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 967
DB 70 AGCCCAAGTGCCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 129
QY 968 CATGAGAGCCCTCTGT 1027
DB 130 CATGAGAGCCCTCTGT 189
QY 1028 TGTGTCCACCTATGAGTGTGAG 1087
DB 190 TGTGTCCACCTATGAGTGTGAG 249
QY 1088 CCTTATGTGGGAG 1147
DB 250 CCTTATGTGGGAG 309
QY 1148 ACAGAAATCTTCTTAATTTTGTCTCAGAAATGAAATTTTGTGAGAGAGAGAGAGAGAGAGAG 1207
DB 310 ACAGAAATCTTCTTAATTTTGTCTCAGAAATGAAATTTTGTGAGAGAGAGAGAGAGAGAGAG 369
QY 1208 CAGGCTCATGTT 1219
DB 370 CAGGCTCATGTT 381

RESULT 11

US-09-960-352-7183
Sequence 7183, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengding
APPLICANT: Byatt, John C.
APPLICANT: Machialagan, Nagappaan
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(1029)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 7183
LENGTH: 421
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 31-LIB3057-014-Q1-K1-H11
US-09-960-352-7183

Query Match 14.38; Score 240.2; DB 10; Length 421;
Best Local Similarity 86.6%; Pred. No. 5.9e-65;
Matches 290; Conservative 0; Mismatches 38; Indels 7; Gaps 2;

QY 3 GGGGCGGTGGTGGGCTAGCGAGCGGAG 61
DB 87 GGGGCGGTGGTGGGAGTCTACCGGTGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 146
QY 62 GCGAGGCGGAGG-----GCGCTTCTTGAATGACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 115
DB 147 GGTGAGGCGGAGCGGAG 206
QY 116 GGTACTGACAGCCAAAG 175

Db 207 GGCCTACTGACGACGAGGAGACTGCGACTGAGAGCTGAGACGACTTCACTGGCGCTAC 266
Qy 176 TCGTAGCTGCGAGGCGCGCGGAGACAGAGACCTGTGGAGTGGAGACACTGAC 235
Db 267 TCGCTGGCGCGGAGCGCGGCTGGAGACAGAGACCGCGTGGAGTGGAGACACTGAC 326
Qy 236 CTTTCTCAAGCTGAGATTGAGACAGAAATCAAGAGATACAAATGCCAGATCAACAGCAAC 295
Db 327 CTTTCTCAAGCTGAGATTGAGACAGAAATCAAGAGATACAAATGCCAGATCAACAGCAAC 386
Qy 296 CTTTCTCAAGCTGAGATTGAGACAGAAATCAAGAGATACAAATGCCAGATCAACAGCAAC 330
Db 387 TTGCTCATGAGCTTGACAGAGATGCGCTCTACAC 421

RESULT 12

US-10-224-356-29
; Sequence 29, Application US/10224356
; Publication No. US20030144196A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: ACTIVATED T LYMPHOCYTE NUCLEIC ACID SEQUENCES AND POLYPEPTIDES EN
; FILE REFERENCE: D0033 NP
; CURRENT APPLICATION NUMBER: US/10/224,356
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/313,957
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 29
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-224-356-29

Query Match 14.2%; Score 238.4; DB 12; Length 795;
Best Local Similarity 60.8%; Pred. No. 3e-64;
Matches 389; Conservative 0; Mismatches 251; Indels 0; Gaps 0;

Qy 210 AGCCTGTGAGTGGAGACACCTGACCTTCTCAAGCTGAGATTGAGAGAAATCAAG 269
Db 131 AACCTGTGAGAGAGACACAGCGCGCCGACACTGAGAGATCAAGAGAAATGAGACA 190
Qy 270 AGTACAATGCCAGATCAACAGCAACCTCTTCATGAGTTGAAGAAGAGCGGTTCTTACA 329
Db 191 GGTACACACGCGAGAGAAAGAACTGCTGGCATGAAACTGAGTGAAGACGGACCTTACA 250
Qy 330 CAGGCTTCATCAAGGTTCAAGTGAAGCTGTGCGCGCTGTCTGTGTGCTCCACAGCAAGA 389
Db 251 CGGGTTTCATCAAAAGTGCATGTGAACCTCGGGGCGCTGTGAAGGTCCTGGCTGGATCC 310
Qy 390 AGCCACCTCTCTTGGCAGAGTGCCTGGCGGGGCCAGAGCGGGCACAACTGTACGGCGCC 449
Db 311 GGCCTCAGTCAAAAGTGCATGTGAACCTCGGGGCGCTGTGAAGGTCCTGGCTGGATCC 370
Qy 330 AGCCACCTCTCTTGGCAGAGTGCCTGGCGGGGCCAGAGCGGGCACAACTGTACGGCGCC 449
Db 311 GGCCTCAGTCAAAAGTGCATGTGAACCTCGGGGCGCTGTGAAGGTCCTGGCTGGATCC 370
Qy 450 GCACCTCTCTTACCTGCGCCCAAGAGTGTCTCAAGCACTGCAATGTGTCTACAGCAAA 509
Db 371 GGACATCTCTTCACTGCGCCCTAGATGCATCAAGAGTGTCTCACTACAGACACACACA 430
Qy 510 GGGCAGCTGAAGTCAATGAGCGCTGCTCGAAAGTCTTGTGTGTGTGATGACACCCGCA 569
Db 431 CGGTCAAGTGAAGTCAATGAGCGCTGCTCGAAAGTCTTGTGTGTGTGATGACACCCGCA 490
Qy 570 AGTTTGACACTCTTTGAGCGCGCTGAGCGTCAAGGCAATGTAAGTGTGCGAAAGCTTTGG 629
Db 491 AGTTTGACACTCTTTGAGCGCGCTGAGCGTCAAGGCAATGTAAGTGTGCGAAAGCTTTCCA 550
Qy 630 ATGATGAGCAGCGCCCTGCGGCTGCGGCTGCTGGCAGAGGCGCAAGTGAACAGGCGCTGAGCT 689
Db 551 TTGCTGACGCGCCCTCTTACCTGCGGCTGCTGTGTGTGTGAGCAGAGAGGTCCTGAGCT 610

Qy 690 TTGCTGAGAGAGAAATGACTGTGGAGGTGAATGGAGCGCTTCACATGCGCTGAAC 749
Db 611 TTGCTGAGAGAGAAATGAACTGGAGAGGTGAAGTGAAGTGGATGCTTCTCATCCCTGAAC 670
Qy 750 TACATACCTCTCTACATATCTGACAGCGGAGAGAGAGAGACACTCTCGCAGATCTCTGC 809
Db 671 TTTCAGACCTTCTTAAACAAATCTGGAAGAGAGAGAGAGCAAAATTCACAAAGTGCAAA 730
Qy 810 AGAATGACTCTCTATGCGCGCCAGAGATCCAAAGAGCGCTT 849
Db 731 AGAATGACTCTCTATGCGCGCCAGAGATCCAAAGAGCGCTT 770

RESULT 13

US-10-224-356-12
; Sequence 12, Application US/10224356
; Publication No. US20030144196A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: ACTIVATED T LYMPHOCYTE NUCLEIC ACID SEQUENCES AND POLYPEPTIDES
; FILE REFERENCE: D0033 NP
; CURRENT APPLICATION NUMBER: US/10/224,356
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/313,957
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 12
; LENGTH: 3389
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-224-356-12

Query Match 14.2%; Score 238.4; DB 12; Length 3389;
Best Local Similarity 60.8%; Pred. No. 6.1e-64;
Matches 389; Conservative 0; Mismatches 251; Indels 0; Gaps 0;

Qy 210 AGCCTGTGAGTGGAGACACCTGACCTTCTCAAGCTGAGATTGAGAGAAATCAAG 269
Db 392 AACCTGTGAGAGAGACACAGCGCGCCGACACTGAGAGATCAAGAGAAATGAGACA 451
Qy 270 AGTACAATGCCAGATCAACAGCAACCTCTTCATGAGTTGAAGAAGAGCGGTTCTTACA 329
Db 452 GGTACACACGCGAGAGAAAGAACTGCTGGCATGAAACTGAGTGAAGACGGACCTTACA 511
Qy 330 CAGGCTTCATCAAGGTTCAAGTGAAGCTGTGCGCGCTGTCTGTGTGCTCCACAGCAAGA 389
Db 512 CGGGTTTCATCAAAAGTGCATGTGAACCTCGGGGCGCTGTGAAGGTCCTGGCTGGATCC 571
Qy 390 AGCCACCTCTCTTGGCAGAGTGCCTGGCGGGGCCAGAGCGGGCACAACTGTACGGCGCC 449
Db 572 GGCCTCAGTCAAAAGTGCATGTGAACCTCGGGGCGCTGTGAAGGTCCTGGCTGGATCC 631
Qy 450 GCACCTCTCTTACCTGCGCCCAAGAGTGTCTCAAGCACTGCAATGTGTCTACAGCAAA 509
Db 632 GGACATCTCTTCACTGCGCCCTAGATGCATCAAGAGTGTCTCACTACAGACACACACA 691
Qy 510 GGGCAGCTGAAGTCAATGAGCGCTGCTCGAAAGTCTTGTGTGTGTGATGACACCCGCA 569
Db 692 CGGTCAAGTGAAGTCAATGAGCGCTGCTCGAAAGTCTTGTGTGTGTGATGACACCCGCA 751
Qy 570 AGTTTGACACTCTTTGAGCGCGCTGAGCGTCAAGGCAATGTAAGTGTGCGAAAGCTTTGG 629
Db 752 AGTTTGACACTCTTTGAGCGCGCTGAGCGTCAAGGCAATGTAAGTGTGCGAAAGCTTTCCA 811
Qy 630 ATGATGAGCAGCGCCCTGCGGCTGCGGCTGCTGGCAGAGGCGCAAGTGAACAGGCGCTGAGCT 689
Db 812 TTGCTGACGCGCCCTCTTACCTGCGGCTGCTGTGTGTGTGAGCAGAGAGGTCCTGAGCT 871
Qy 690 TTGCTGAGAGAGAAATGACTGTGGAGAGTGAATCTGGACAGCTTCAAGATGCTGAAAC 749
Db 872 TTGCTGAGAGAGAAATGAACTGGAAGGTGAAGTGGATGCTTCTCATCCCTGAAC 931

Db 1014 AGAAGTATGACAAAGTTTAGGCGAGAACTGGAGGAGGCCCTT 1053

Search completed: August 20, 2003, 09:51:42
Job time : 421.945 secs

THIS PAGE BLANK (USPTO)